

# FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCCG  
CAGCGCTACCCGCCATGCCGCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG  
CTGCTGCCGCCC GCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT  
GGTGGACAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACA  
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATC  
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTTCGAGTGGTTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCC GACTGTCTCGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA  
GGGCGACGGGTCTTCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT  
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG  
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA  
CGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACG  
AAAAGTGTACAATACTCCAGGGAGCTACGTCTGTGTGTGTCTTGACGGCTTCGAAGAAACG  
GAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT  
GCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTACCCTTTAAATTATTTCAGAAGGATGTCC  
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGGAGAGGCTGC  
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTGTTCTTA  
AACAGACTTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGG  
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC  
TTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCA  
TCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC  
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTCGGCGCAGCACCATGGCCTGAAAT  
AACCTCTGAAAGAGGAACTTGGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG  
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTTT

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Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
Male	55.2 (10.5)
Female	56.8 (11.2)
Marital status	
Married	78.5%
Single	21.5%
Education level	
High school or above	65.2%
Below high school	34.8%
Occupation	
Professional	12.3%
Managerial	18.7%
Technical	25.4%
Service	31.2%
Unemployed	12.4%
Income (USD/month)	
< 1000	15.6%
1000-2000	28.9%
2000-3000	35.7%
> 3000	19.8%

><MW: 38192, pI: 4.53, NX(S/T): 2

**Signal peptide:**

N-glycosylation sites.

Glycosaminoglycan attachment sites.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

### Casein kinase II phosphorylation sites.

**Tyrosine kinase phosphorylation site.**

N-myristoylation sites.

Aspartic acid and asparagine hydroxylation site.

**EGF-like domain cysteine pattern signature.**

Leucine zipper pattern.

amino acids 94-116

### FIGURE 3

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CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG  
GCACGAGGAGTTTTTCCCGGCAGCGAGGAGGTCCTGAGCAGCATGCCCCGGAGGAGCGCCTTC  
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGC  
CGGGCCGCCGAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA  
TAGGATTTGAAGAAGATATCCTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGAT  
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCTTGGCGCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA  
TCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAACAGGATGGGGTGGCAGCATTGGAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAAATGCTATCT  
TCTTTAAAACATGTCAACAAGCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAAT  
GAAAGACGCATCTGCGAGTGTCTGATGGGTTCACGGACCTCACTGTGAGAAAGCCCTTTG  
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG  
GATTCTATGGAGTGAAGTGTGACAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGGACC  
TGTTTCTACCCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
CAAATGCCCACAACCCCTGTGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTT  
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACAT  
GGAACCTGCCATGAACCCCAACAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC  
ACACGCCTTCACTTAAAAAGGCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGG  
TGAACTCCGACATCTGAAACGTTTTAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTCA  
TGTGTTGAATGTTCAAATAATGTTTATTACACTTAAGAATACTGGCCTGAATTTTATTAGCT  
TCATTATAAATCACTGAGCTGATATTTACTCTTCCTTTTAAGTTTTCTAAGTACGTCTGTAG  
CATGATGGTATAGATTTTCTTGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA  
TCAGGTTAAAATTTTCAGTGTGTAGTTGGCAGATATTTTCAAATTTACAATGCATTTATGGT  
GTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAAGAAT  
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTCAGATTTTATTGTCAGATATTTAGAT  
GTTTGTTACATTTTAAAAATTGCTCTTAATTTTAAACTCTCAATACAATATATTTTGACC  
TTACCATTATTCCAGAGATTCAGTATTAACAAAAAAAAAAAAATTACACTGTGGTAGTGGCATT  
AAACAATATAATATATTCTAAACACAATGAAATAGGGAATATAATGTATGAACTTTTTGTCAT  
TGGCTTGAAGCAATATAATATATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTAT  
ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC  
CGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

## **FIGURE 4**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094

><subunit 1 of 1, 379 aa, 0 stop

><MW: 41528, pI: 7.97, NX(S/T): 2

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK  
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL  
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGC  
RNGGFCNERRICECPDGFHGHPCKEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST  
TCFNGGTCFYPPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSPVC  
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERDRP  
PESNYIW

### **Signal peptide:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 88-92, 245-249

### **Casein kinase II phosphorylation site.**

amino acids 319-323

### **Tyrosine kinase phosphorylation site.**

amino acids 370-378

### **N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

### **ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

### **EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTTCGACAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG  
CCCCAGCCCACACCTTCACCAGGGCCCAGGAGCCACC**ATGT**TGGCGATGTCCACTGGGGCTAC  
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCCAGCAGGGTCGTGGGCGCCGG  
GAGCTAGCACCGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT  
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC  
TGCCTCGGCGTGCCACCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCTGATCTA  
TCCAGTCTTGGGAACGTACTGGGACAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT  
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACCACAGCGCCTTCTGGGGCATGACCCTGGAT**G**AGGGCATTCTGCTACCGCCTGGGCACCA  
TCCGCCCATCTTCCTCGGTTCATGAACATGCATGAAATTTATACAGTGTGAACCCAGGGGAG  
GTGCTTCCACAGCCTTCGAGGCCTCTGAGAAAGTGGCCCAACCTGATTCATGAGCCTCTTGA  
CCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT  
CAATCCATTCTCTGGGACACATGACGCCTGTCTGTGCGCCCCAGAACCCTGCTGTCTTGTGAC  
ACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCCG  
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC  
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCC  
CACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA  
TGGAGGTGCATGAGGACTTCTTCTATAACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATAACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG  
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCCTGGGGCC  
CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGC GCGGCGTCAATGAGTGCGACATCGAG  
AGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTTCATCACTGAGGCTG  
CGGGCACACGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG  
GGGCGGTGACCCCAGCCTCGCCCGACAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAAT  
CCCGGCGCGGGTTCCGCTGACGACGCGCCCCGCTGGGAGCCGCGGGCAGGCGAGACTGGCG  
GAGCCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCAG  
ATCCAGGCCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC  
CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG  
TTGCCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA  
AGTGACCCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACCACACCTGGC  
TAATTTTTGTATTTTTGTAAAGAGGGGGGTCTCACTGTGTTGCCCAGGCTGGTTTCGAACT  
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTGCTGGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAAA  
TAAAACCAAAGTATTGATAAAAAAAA

## **FIGURE 6**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC

ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNR

CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

### **N-glycosylation site.**

amino acids 78-82, 161-165

### **Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

### **N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

### **Amidation site.**

amino acids 26-30, 318-322

### **Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

Figure 6

## FIGURE 7

AGGCTCCTTGGCCCTTTTTCCACAGCAAGCTTNTGCNATCCCGATTTCGTTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCTGTCCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC  
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACCTCCTGTCTACCGCCTCGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG  
TGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG  
AGGCCAGAGAGATAACCGCCGGCATGGGACCCACTCAG

000445.01.2940660

## **FIGURE 8**

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG  
CAGCTTGAAGTGCCTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT  
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCCAGTGGGAGCCTGTCTTGGTTCTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCCACCCTGACCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCTCTCTGCTGCTGTTTC  
CATGGCCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT  
CCCTGCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA  
GGGGACAGGCACTCAGGAGGGGCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA  
GGACAAGAGTCGACGTGAGTTCCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTCGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAA

TCCTAGTACACAGATCCGCCTGCAGATGGCCCTCCAACCCTCTCTGCTGCTGTTTC



## **FIGURE 9**

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPSSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPMPMALSRTPTRQISSDT  
DPPADGPSNPLCCCFHGPAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

### **Signal peptide:**

amino acids 1-47

### **N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

### **Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

### **N-myristoylation site.**

amino acids 56-60

### **Amidation site.**

amino acids 70-74

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## **FIGURE 10**

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCGCCTGCTGCCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC  
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGCAGGTACACGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC  
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTG  
CGTGTTACGGAGATCGTGCTGGAGAACAACCTATACGGCCTTCCAGAACGCCCCGGCACGAGG  
GCTGGTTCATGGCCTTCACGCGGCAGGGGCGGCCCCGCCAGGCTTCCCGCAGCCGCCAGAAC  
CAGCGCGAGGCCCACCTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCCACGC  
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCCACC CGCCGGACCAAGCGCACAC  
GGCGGCCCCAGCCCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCCCTGGGCGCCTCCC  
CACCCCTTTCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC  
GAGGGAGGACCCTGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTG  
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT  
GAGTGTCACCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCCAGCCGGGCTCCTGAAGCC  
CGCTGAAAGGTACGCGACTGAAGGCCTTGACAGACAACCGTCTGGAGGTGGCTGTCTCAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTA  
GGAAGGGACTTTTGTTTGTGTTTGTGTTTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAATAG  
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCCACCCCCAACTCCCAGCCC  
CGGAATAAAACCATTTTTCCTGC

## **FIGURE 11**

MGAARLLPNLTLCQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDCVFTEIVLENNYTAFQONARHEGWFMATFTRQGRPRQASRSRQNRQREAHFIKRLYQGQLPFPNHAEKQKQFEFVGSAPTRRTKRTRRPQPLT

### **Signal peptide:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 9-13, 126-130

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

### **Casein kinase II phosphorylation site.**

amino acids 65-69

### **Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

### **N-myristoylation site.**

amino acids 69-75, 188-194

### **Amidation site.**

amino acids 58-62

### **HBGF/FGF family signature.**

amino acids 103-128

## FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT  
CATTTTGATTTTGCTGTTTATTTTTTTTTCTTTTTCTTTTTCCCACCACATTGTATTTTAT  
TTCCGTACTTCAGAAATGGGCTACAGACCACAAAGTGGCCCAGCCATGGGGCTTTTTTCTT  
GAAGTCTTGGCTTATCATTTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC  
CTAGTGTGTGCCGCTGCGACAGGAACCTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG  
CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC  
TGGATTTCTTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC  
AACTGGACGAATTCCTCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTGTCAGGAAAAAC  
AATATTCAGACCATTTCACGGGCTGCTCTTGGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT  
GGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC  
TCAAATTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCTATATCCGACATGGCCTTCCAGAA  
TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG  
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCC  
CACCTCCTCCCGATCTCCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACCAGAT  
AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCTTTGGTTTTGTGACTGCAGTATTAAATGGGTACAGAAATGGCTCAA  
ATATATCCCTTCATCTCTCAACGTGCGGGGTTTTCATGTGCCAAGGTCTGAACAAGTCCGGG  
GGATGGCCGTCAGGGAATTAATATGAATCTTTTGTCTGTCCCACCACGACCCCCGGCCTG  
CCTCTCTTACCCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCTCTCTAT  
TCCAAACCTTAGCAGAAGCTACACGCCTCCAACCTCCTACCACATCGAAACTTCCCACGATTC  
CTGACTGGGATGGCAGAGAAAGAGTGACCCCACTATTCTGAACGGATCCAGCTCTCTATC  
CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTACCGTGATGGCATA  
CAAACCTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGCATCGTTCAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAGAGGC  
CACCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT  
GTGCTGGTGGTCTTGCTCAGCGTCTTTTGTGCTGGCATATGCACAAAAAGGGGCGCTACACCTC  
CCAGAAGTGGAATAACAACCGGGGCGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA  
AGGACAACTCCATCCTGGAGATGACAGAAACCAGTTTTTCAGATCGTCTCCTTAAATAACGAT  
CAACTCCTTAAAGGAGATTTTCAGACTGCAGCCCATTTACACCCCAAATGGGGGCATTAATTA  
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC  
ACTGCCATACGTTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA  
CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT  
TTGTGCATTTGAATACTCTGTAAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG  
CTATCTTTCTATTTCAAGTTAATTACAAACAGTTTTGTAACTCTTTGCTTTTTTAAATCTT

## **FIGURE 13**

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP  
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI  
SRAALAQLLKLEELHLDDNSISTVGVEDGAFREAISLKLFLSKNHLSSVPVGLPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD  
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN  
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMVRELNMMNLLSCPTTTPGLPLFTP  
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPISERIQLSIHFVND  
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL  
DAFNRAVEDTICSEATTHASYLNNGSNTASSHEQTTSMSGSPFLLAGLIGGAVIFVLVVL  
LSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG  
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## FIGURE 14

ACTTGGAGCAAGCGGCGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCTCGCCTCCCACGAGCG  
ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCCCTGCC  
TCGCTTCCCAGGCGCCGCGGCTGCGAGCCTTGCCCCCTTTGCTCGCCTTGAAAATGGAAAAGATGCTCGCAGGCT  
GCTTTCTGCTGATCCTCGGACAGATCGTCTCTCCCTGCCGAGGCCAGGGAGCGGTACGCTGGGAGGTCCATCT  
CTAGGGGCGAGACACGCTCGGACCCACCCGACAGCGGCCCTTCTGGAGAGTTCTGTGAGAACAAAGCGGGCAGACC  
TGGTTTTTCATTCATTGACAGCTCTCGAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTTCATCGTGGACA  
TCTTGCAATTCTTGGACATTGGTCTGATGTCAACCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGAATG  
AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGTGTCAAGAGGATGCGGCATCTGTCCACGG  
GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTTCTCAGAAGCAGAGGGGGCCCCGGCCCCCTGA  
GGGAGAATGTGCCACGGGTCTAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGCTGCTA  
AGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG  
GGAGTGAGCCCCATGAGGACCATGTCTTCTTGTGGCCAAATTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC  
AGAAGAAGTTGTGCACGGGCCACATGTGCAGCACCCCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTG  
GCTCATACGTCTGCAGGTGCAACAAGGCTACATTTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT  
GTGCCATGGAGGACCACAACGTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCTTCGTCTGCCAGTGCTACAGTG  
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAAAACACGGATGTGAAC  
ATGAGTGTGTAAATGCTGATGGCTCCTACCTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAA  
CGTGCACAAGGATCAACTACTGTGCATGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT  
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAAACCTGCAGCCGAGTGGACCACTGTGCAC  
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCCTTCGTCTGCCAGTGCTCAGAAGGCTTCC  
TCATCAACGAGGACCTCAAGACCTGCTCCCGGTGGATTACTGCCTGCTGAGTGACCATGGTTGTGAATACTCCT  
GTGTCAACATGGACAGATCCTTTGCCTGTCACTGTCTTGAGGACACGCTGCTCCGCAGCGATGGGAAGACGTGTG  
CAAAATTGGACTCTTGTGCTCTGGGGGACCACGGTTGTGAACATTCGTGTGTAAGCAGTGAAGATTCGTTTGTGT  
GCCAGTGCTTTGAAGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTATAG  
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACACGTGCGAGTGCTTGGAGGGATTCCGGCTCG  
CTGAGGATGGGAACGCTGCCGAAGGAAGGATGTCTGCAAAATCAACCCACCATGGCTGCGAACACATTTGTGTTA  
ATAATGGGAATTCTTACATCTGCAAAATGCTCAGAGGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAAT  
GCACTGAAGGCCCAATTGACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAAGAGAGAAATTTTGAGGTCCG  
TGAAGCAGTTTGTCACTGGAATTATAGATTCCTTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGT  
ATTCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCAACTCAGCCAAAGACATGAAAAAAGCCGTGGCCC  
ACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAAGTTTACCCAAAG  
GAGAAGGGGCCAGGCCCTTTCCACAAGGGTGCCGAGAGCAGCCATTGTGTTACCCGACGGACGGGCTCAGGATG  
ACGTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG  
AGGAGGAACACAAGAGATTGCCCTCTGAGCCCAAAACAAGCATCTTCTATGCCGAAGACTTCAGCACAAATGG  
ATGAGATAAGTAAAAAATCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG  
CAGGGGAACCTGCCAAAAACGGTCCAACAGCCAACAGAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT  
CCTGTTCTAATTTTGCAGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTT  
CCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAAAATGTGAAAACCTTATAATGT  
TCCAGAACCTTGCAAACGAAGAAGTAAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC  
TGGAAAATCGCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTATCACGGATTACAAT  
GAACGCAGTGCAGAGCCCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTGA  
GAAACCTGGTTTGGCACAGAACAAGACAAGAAGTATACACTAACTTGTATAAATTTATCTAGGAAAAAATCCT  
TCAGAATTTAAGATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAATATACTGTGGACAC  
AACTTGCTTCTGCCTCATCCTGCCTTAGTGTGCAATCTCATTTGACTATACGATAAAGTTTGCACAGTCTTACTT  
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTTGTACTGGACTTTACCTTGATATATGTATATGGATGTATG  
CATAAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTTATACAATATTAATAATTCACCACTTCAG

FIGURE 14

## **FIGURE 15**

MEKMLAGCFLILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFII  
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV  
KRMRLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD  
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN  
CAHFCINIPGSYVCRCKQGYILNSDQTTTCRIQDLCAMEDHNCQQLCVNVPGSFVCQCYSGYA  
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINICALNKP GC  
EHECVNMEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQ CSEGFLI  
NEDLKTC SRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTC AKLDS CALGDHGCE  
HSCVSSSEDSFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLA  
EDGKRCRRKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVID  
GSKSLGEENFEVVKQFVTGIIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA  
HMKYMGKGSMTGLALKHMFERSFTQEGGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEEELQEIASEPTNKHLYAEDFSTMD EISEKLKKGICEALEDSDGRQDS  
PAGELPKTVQQPTESEPTVINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL  
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

### **Signal peptide:**

amino acids 1-23

### **N-glycosylation site.**

amino acids 221-225

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

### **Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

### **N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

### **Amidation site.**

amino acids 314-318, 560-564, 601-605

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGC  
CATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA  
GTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAG  
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGGAGGTGTCTTC  
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC  
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT  
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT  
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG  
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC  
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT  
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCAT  
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT  
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAAGCTGGCTCTCTGGTATGATGAC  
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCAC  
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC  
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC  
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC  
TTATTAAACTAACATGAAATATGTGTTGTTTTTCATTTGCAAATTTAAATAAAGATACATAA  
TGTTTGTATGAAAAA



## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPVGVGANVTLSQCQSPRSKPAVQYQ  
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA  
VVAGAVVGTILVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL  
SSVTSARALRPPHGPFRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

### **Signal peptide:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 245-267

### **N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

### **N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	22	55
Gender	0.5	0.5	0	1
Marital Status	0.6	0.5	0	1
Education	12.5	1.5	10	15
Income	3500	1500	1000	7000
Health	0.8	0.2	0	1
Smoking	0.3	0.5	0	1
Alcohol	0.2	0.4	0	1
Exercise	0.4	0.5	0	1
Stress	0.6	0.5	0	1
Depression	0.3	0.5	0	1
Loneliness	0.4	0.5	0	1
Life Satisfaction	0.7	0.3	0	1
Quality of Life	0.8	0.2	0	1
Overall Health	0.9	0.1	0	1
Physical Health	0.9	0.1	0	1
Mental Health	0.8	0.2	0	1
Social Health	0.7	0.3	0	1
Emotional Health	0.6	0.4	0	1
Behavioral Health	0.5	0.5	0	1
Environmental Health	0.4	0.5	0	1
Occupational Health	0.3	0.5	0	1
Financial Health	0.2	0.4	0	1
Family Health	0.1	0.3	0	1
Community Health	0.0	0.2	0	1
National Health	0.0	0.1	0	1
Global Health	0.0	0.0	0	1

CGCAACCACTGCCGGCCACGCCAAATGCAAAACGCTCTCCGCTCCTAGTAGTGGTTTTTTTCCACTTTTG  
TTGAATTGTTCCTATACTCAAATTTGCACCAAGACACCTTGTCTCCCAAATGCAAAATGTGA  
AATACGCAATTGGAATTGAAGCCTGCTATTGCAACATGGGATTTTCAGGAAATGGTGTCA  
TTTGTGAAGATGATAATGAATGTGGAAATTTAACTCAGTCCTGTGGCGAAAATGCTAATTGC  
ACTAACACAGAAGGAAGTTATTATTGTATGTGTGTACCTGGCTTCAGATCCAGCAGTAACCA  
AGACAGGTTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATT  
TAGATAATGTCTGTATAGCTGCAAATATTAATAAAACTTTAACAAAAATCAGATCCATAAAA  
GAACCTGTGGCTTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTTCACCAACAGA  
TATAATTACATATATAGAAATATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAACA  
CTATCTCAGCCAAGGACACCCCTTTCTAACTCAACTCTTACTGAATTTGTA AAAACCGTGAAT  
AATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATAGGAGAAC  
ACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCAGAGCTTCC  
AAAAGACCACAGAGTTTGATACAAATTCACGGATATAGCTCTCAAAGTTTTCTTTTTTGAT  
TCATATAACATGAAACATATTCATCCTCATATGAATATGGATGGAGACTACATAAATATATT  
TCCAAAGAGAAAAGCTGCATATGATTCAAATTGCAATGTTGCAGTTGCATTTTTTATATTATA  
AGAGTATTGGTCCTTTGCTTTCATCATCTGACAACCTCTTATTGAAACCTCAA AATTATGAT  
AATCTGAAGAGGAGGAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC  
ACCCACATTATATGAACTTGAAAAATAACATTTACATTAAAGTCATCGAAAGGTCACAGATA  
GGTATAGGAGTCTATGTGCATTTTGAATTACTCACCTGATACCATGAATGGCAGCTGGTCT  
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT  
GACACATTTTGCAATTTTGATGTCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTC  
TTACAAGGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTT  
ACCTTCTGGTTCTTCAGTGAAATTCAAAGCACCCAGGACAACAATTCACAAAAATCTTTGCTG  
TAGCCTATTTCTTGCTGAACTTGTTTTTCTTGTTGGGATCAATACAAATACTAATAAGCTCT  
TCTGTTCAATCATTGCCGAGCTGCTACACTACTTCTTTTTAGCTGCTTTTGCATGGATGTGC  
ATTGAAGGCATACATCTCTATCTCATTGTTGTGGGTGTCATCTACAACAAGGGATTTTTTGCA  
CAAGAATTTTTATATCTTTGGCTATCTAAGCCCAGCCGTGGTAGTTGGATTTTCGGCAGCAC  
TAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCGAAAAACAAC TTTATT  
TGGAGTTTTATAGGACCAGCATGCCTAATCATTCTTGTTAATCTCTTGGCTTTTGGAGTCAT  
CATATACAAAGTTTTTCTGTCACACTGCAGGGTTGAAACCAGAAAGTTAGTTGCTTTGAGAACA  
TAAGGTCTTGTGCAAGAGGAGCCCTCGCTCTTCTGTTCTTCTCGGCACCACCTGGATCTTT  
GGGGTTCTCCATGTTGTGCACGCATCAGTGGTTACAGCTTACCTCTTCACAGTCAGCAATGC  
TTTCCAGGGGATGTTCA TTTTTTTTATTCTCTGTGTGTTTTATCTAGAAAGATTCAAGAAGAAT  
ATTACAGATTGTTCAA AATGTCCCCTGTTGTTTTGGATGTTTAAAGGTAAACATAGAGAATG  
GTGGATAATTACAACCTGCACAAAAATAAAAATTTCCAAGCTGTGGATGACCAATGTATAAAAA  
TGACTCATCAAATTATCCAATTATTAAC TACTAGACAAAAAGTATTTTTAAATCAGTTTTTCT  
GTTTATGCTATAGGAACTGTAGATAATAAGGTAAAAATTATGTATCATATAGATATACTATGT  
TTTTCTATGTGAAATAGTTCTGTCAAAAATAGTATTGCAGATATTTGGAAAGTAATTGGTTT  
CTCAGGAGTGATATCACTGCACCCAAGGAAAGATTTTCTTTCTAACACGAGAAGTATATGAA  
TGTCTTGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTTGCCTTTGAAACTAGTCC  
CCTACCACCTCGGTAAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAATGAAGGGGCAGA  
ATATCAAACAGTGAAAAGGGAATGATAAGATGTATTTTGAATGAACTGTTTTTTCTGTAGAC  
TAGCTGAGAAATTGTTGACATAAAAATAAAGAATTGAAGAAACACATTTTACCATTTTGTGAA  
TTGTTCTGAACTTAAATGTCCACTAAAACAAC TTAGACTTCTGTTTGCTAAATCTGTTTTCTT  
TTTCTAATATTCTAAAAA AAAAAAAAAAAGGTTTACCTCCACAAATTGAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 19**

MKRLPLLVPFSTLLNCSYTONCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENTVNANCHLDNVCIAA  
NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL  
SNSTLTETVKTNNFVQRDTFVWWDKLSVNHRRTHLTKLMHTVEQATLRISQSFQKTTEFDT  
NSTDIALKVFFFDSDYNMKHIHPHMNDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS  
SSDNFLLKPQNYDNSEEEERVISVISVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAF  
WNYSPTMNGSWSSEGCELTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG  
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSTIIAGL  
LHYFFLAFAWMCIEGHLVYLVGVIYNKGFLHKNFYIFGYLSPAVVVGFSALGYRYYGT  
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVLHVHVSVVTAFLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV  
PCCFGCLR

### **Signal peptide:**

amino acids 1-19

### **Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

### **N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

### **Glycosaminoglycan attachment site.**

amino acids 49-53

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

### **Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

### **Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

### **N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## **FIGURE 20**

TGGAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT  
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCCACCCAC  
ATTATATGAACTTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA  
GGAGTCTATGTGGCATTTTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTTACCTTC  
TGTTCTTCAGTGAAATTCAAAGCACCAGGA

FIGURE 20

## FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG  
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCGGCTGGGA  
CAAGAAGCCGCCGCTGCTGCCCCGGGCCCGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG  
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG  
TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCGGAG  
CCGCCGCGCCGTGAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC  
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCATCGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC  
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCC  
ACGGGCTCTCCAGCTGCTTCCCTGCGCATCCGTGCCGACGCGCTCGTGGACTGCGCGCGGGGC  
CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG  
CGTGACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTTGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA  
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA  
CAGAGGCTTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCCCTGGAGACCGACAGCATG  
GACCCATTTGGGCTTGTACCGGACTGGAGGCCGTGAGGAGTCCCAGCTTTGAGAAGTAACT  
GAGACCATGCCCCGGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG  
TGCTTCTACAAGAACAGTCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA  
GTTGTACATATTGAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT  
CATAACATTGTAAGCCTGTAGCTTGCCCAGCTGCTGCCTGGGCCCCCATTTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC  
TCACTTCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC  
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTAGGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG  
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCACCAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAATTCCCC  
CTGAGGCCAGTTCTGTGATGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGTACCTGC  
TTCCATCTCCCAGCCCACCAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGGCCT  
CCCAGGCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGAAGACCTAGAAC  
CCTTTCCCAGCACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA  
TCTCTTATTTTCTTACATTATTTATGCCCCCAAATTATATTTATGTATGTAAGTGAGGTTTG  
TTTTGTATATTAAATGGAGTTTGTGTGT

## **FIGURE 22**

MRS GCVVHVWILAGLWLA VAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLEIKAV ALRTVAIKGVH SVRYLCMGADGKMQGLLQYSEEDCAFEE  
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

### **Signal peptide:**

amino acids 1-22

### **Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

### **N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

TOP 20" 29440660

Variable	Mean	Standard deviation	Minimum	Maximum
Age	34.5	10.5	20	65
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	2.5	9	16
Income	15.5	5.5	10	25
Health status	0.5	0.5	0	1
Smoking status	0.5	0.5	0	1
Alcohol consumption	0.5	0.5	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.5	0.5	0	1
Life satisfaction	0.5	0.5	0	1
Depression score	0.5	0.5	0	1
Loneliness score	0.5	0.5	0	1
Quality of life score	0.5	0.5	0	1
Healthcare utilization	0.5	0.5	0	1
Health insurance status	0.5	0.5	0	1
Healthcare access	0.5	0.5	0	1
Healthcare cost	0.5	0.5	0	1
Healthcare quality	0.5	0.5	0	1
Healthcare satisfaction	0.5	0.5	0	1
Healthcare utilization (continued)	0.5	0.5	0	1
Health insurance status (continued)	0.5	0.5	0	1
Healthcare access (continued)	0.5	0.5	0	1
Healthcare cost (continued)	0.5	0.5	0	1
Healthcare quality (continued)	0.5	0.5	0	1
Healthcare satisfaction (continued)	0.5	0.5	0	1

Variable	Mean	Standard deviation	Minimum	Maximum
Age	34.5	10.5	20	55
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	1.5	10	15
Income	15.5	5.5	10	25
Health status	0.5	0.5	0	1
Smoking status	0.5	0.5	0	1
Alcohol consumption	0.5	0.5	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.5	0.5	0	1
Sleep quality	0.5	0.5	0	1
Work satisfaction	0.5	0.5	0	1
Life satisfaction	0.5	0.5	0	1
Overall health	0.5	0.5	0	1
Physical activity	0.5	0.5	0	1
Mental health	0.5	0.5	0	1
Social support	0.5	0.5	0	1
Work-life balance	0.5	0.5	0	1
Financial stability	0.5	0.5	0	1
Family harmony	0.5	0.5	0	1
Personal growth	0.5	0.5	0	1
Community involvement	0.5	0.5	0	1
Environmental awareness	0.5	0.5	0	1
Cultural appreciation	0.5	0.5	0	1
Artistic expression	0.5	0.5	0	1
Volunteer work	0.5	0.5	0	1
Charitable contributions	0.5	0.5	0	1
Philanthropic activities	0.5	0.5	0	1
Leadership roles	0.5	0.5	0	1
Networking opportunities	0.5	0.5	0	1
Professional development	0.5	0.5	0	1
Continuous learning	0.5	0.5	0	1
Adaptability to change	0.5	0.5	0	1
Resilience to stress	0.5	0.5	0	1
Emotional regulation	0.5	0.5	0	1
Conflict resolution skills	0.5	0.5	0	1
Effective communication	0.5	0.5	0	1
Team collaboration	0.5	0.5	0	1
Problem-solving abilities	0.5	0.5	0	1
Decision-making skills	0.5	0.5	0	1
Time management	0.5	0.5	0	1
Organization skills	0.5	0.5	0	1
Attention to detail	0.5	0.5	0	1
Initiative and proactivity	0.5	0.5	0	1
Accountability	0.5	0.5	0	1
Integrity and honesty	0.5	0.5	0	1
Empathy and compassion	0.5	0.5	0	1
Respect for others	0.5	0.5	0	1
Open-mindedness	0.5	0.5	0	1
Curiosity and exploration	0.5	0.5	0	1
Creativity and innovation	0.5	0.5	0	1
Perseverance and persistence	0.5	0.5	0	1
Optimism and positivity	0.5	0.5	0	1
Gratitude and appreciation	0.5	0.5	0	1
Humility and modesty	0.5	0.5	0	1
Patience and tolerance	0.5	0.5	0	1
Self-discipline and focus	0.5	0.5	0	1
Goal setting and achievement	0.5	0.5	0	1
Resilience to setbacks	0.5	0.5	0	1
Adaptability to challenges	0.5	0.5	0	1
Proactive problem-solving	0.5	0.5	0	1
Effective time management	0.5	0.5	0	1
Organization and planning	0.5	0.5	0	1
Attention to detail and accuracy	0.5	0.5	0	1
Initiative and proactivity	0.5	0.5	0	1
Accountability and responsibility	0.5	0.5	0	1
Integrity and honesty	0.5	0.5	0	1
Empathy and compassion	0.5	0.5	0	1
Respect for others	0.5	0.5	0	1
Open-mindedness	0.5	0.5	0	1
Curiosity and exploration	0.5	0.5	0	1
Creativity and innovation	0.5	0.5	0	1
Perseverance and persistence	0.5	0.5	0	1
Optimism and positivity	0.5	0.5	0	1
Gratitude and appreciation	0.5	0.5	0	1
Humility and modesty	0.5	0.5	0	1
Patience and tolerance	0.5	0.5	0	1
Self-discipline and focus	0.5	0.5	0	1
Goal setting and achievement	0.5	0.5	0	1
Resilience to setbacks	0.5	0.5	0	1
Adaptability to challenges	0.5	0.5	0	1
Proactive problem-solving	0.5	0.5	0	1
Effective time management	0.5	0.5	0	1
Organization and planning	0.5</			

## **FIGURE 24**

MARRSRHRLLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE  
WKKLGRSVSFVYYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNL EED  
TVTLEVLVAPAVPSCCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST  
NSSYTMNTKTGT LQFNTVSKLDTGEYSCEARN SVGYRRC PGKRMQVDDL NISGIIAAVVVVA  
LVISVCGLGVCYAQRKGYFSKETS FQKSNSSSKATTMS ENVQWLTPVIPALW KAAAGGSRGQEF

### **Signal peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 130-144, 238-258

### **N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

### **Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

### **N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

### **Amidation site.**

amino acids 226-230

PROTEIN 23440660



## FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG  
AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCCTGGCAT  
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA  
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA  
TTATATCATTAAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTTTGGACAATG  
CAATTGTGGCACTGGCACTTATTTTCAGTGAAGAAAAACTTTGTGGTTCTATGGCATTTCATCA  
TTTGACAAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTG  
TGGAATCCTTAAGGGCCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG  
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTTAT  
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCAGATTGCC  
AGCTAACACACAGATTCTTCTCCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAG  
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTTATCTTCAGTCACCAAT  
ATTAATGTAAAAAAGATGCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAACAACTTACTGA  
ACTGCCTGAAAAATGTCTGTCCGAAGTGAAGCACTTACAAGAACTCTATATTAATCACAAC  
TGCTTTCTACAATTTACCTGGAGCCTTTATTGGCCTACATAATCTTCTTCGACTTCATCTC  
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAGAGAT  
TCTGATGATTGGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAAGCCTCTTATCA  
ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTT  
GGACTGGAAAACCTAGAAAGCATCTCTTTTACGATAACAGGCTTATTAAAGTACCCCATGT  
TGCTCTTCAAAAAGTTGTAAATCTCAAATTTTGGATCTAAATAAAAAATCCTATTAATAGAA  
TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGATAAATAATATGCCT  
GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC  
TACTAACAAACCCTAGATTGTCTTACATTACCCCCATATGTCATTTTTCAGACTCCCCAAGCTGG  
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG  
CCAAACCTCAAGGAAATCAGCATAACAGTAACCCCATCAGGTGTGACTGTGTCTATCCGTTG  
GATGAACATGAACAAAACCAACATTCGATTCATGGAGCCAGATTCACTGTTTTGCGTGGACC  
CACCTGAATTCGAAGGTGAGATGTTTCGGCAAGTGCATTTTCAGGGACATGATGGAAATTTGT  
CTCCCTCTTATAGCTCCTGAGAGCTTTCTCTTAATCTAAATGTAGAAGCTGGGAGCTATGT  
TTCCTTTCAGTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTG  
GTCAAAAACCTCTTGCCTAATACCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA  
GATATAAATGGCGTAACCTCCCAAAGAAGGGGGTTTATATACTTGTATAGCAACTAACCTAGT  
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG  
GCTCTTTGAATATTTAAATAAGAGATATTCAGGCCAATTCAGTTTTTGGTGTCTTGGAAAGCA  
AGTTCTAAATTTCTCAAATCTAGTGTAAATGACAGCCTTTGTCAAGACTGAAAATTCTCA  
TGCTGCGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTTGTATTGATATTTCCACCATCTATCAGAAAAACAGAAAAAAA  
TGTGTAAATGTCAACCACCAAAGGTTTGCACCCTGATCAAAAAGAGTATGAAAAGAATAATAC  
CACAACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA  
GCTGCCTCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG  
AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA  
AGAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTATAGGTTTACCAACAAATATGTCTT  
AAAAACCAAGGAAACCTACTCCAAAAATGAAC

## **FIGURE 26**

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT  
FPARLPANTQILLQLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTPEKCLSELNLQELYINHNLSTISPGAFIHLNLLRLHLNSNRLQMINSKWFDA  
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRL  
IKVPHVALQKVNLKFLDLNKNPINRIRRGDFSNNLHLKELGINNMPELISIDSLAVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHNPIRC  
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGNVRQVHFRDMMEICLPLIAPESFPSNLNV  
EAGSYVSFHCRTAEPEIYWITPSGQKLLPNTLTDFYVHSEGTLDINGVTPKEGGLYTC  
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFAV  
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE  
YEKNNTTTLMACLGGLLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPPPLIN  
LWEAGKEKSTSLKVKATVIGLPTNMS

### **Signal sequence:**

amino acids 1-22

### **Transmembrane domain:**

amino acids 633-650

### **N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

### **Tyrosine kinase phosphorylation site.**

amino acids 570-579

### **N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

### **Cell attachment sequence.**

amino acids 277-280

## **FIGURE 27**

GCCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC  
CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT  
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTA  
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGG  
GGTTTAAATGTACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAG  
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT  
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC  
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC  
CAACGACGCTGACCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG  
GATGCCCCGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTATTAGTGTCCAACTGACTGTCATTGAGAAAGAAAGAAA  
GTAGTTTGCGATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA  
ACTTTGTATTTTCAGTTTTTTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACA  
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT  
AATTTAAAGCAAATAAAAGCTTAACCTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	0.45	0.50	0	1
Marital status	0.60	0.49	0	1
Education	12.5	1.5	9	16
Income	15.2	8.5	5	35
Health status	0.75	0.43	0	1
Stress level	2.5	1.2	1	4
Life satisfaction	3.8	1.5	1	5
Work engagement	4.2	1.0	1	5
Organizational commitment	4.5	1.1	1	5
Job satisfaction	4.0	1.2	1	5
Turnover intention	1.5	1.0	0	3
Organizational citizenship behavior	3.5	1.0	1	5
Employee well-being	3.2	1.1	1	5
Work-life balance	3.0	1.2	1	5
Job stress	2.8	1.0	1	4
Organizational trust	4.0	1.0	1	5
Employee engagement	4.1	1.1	1	5
Job performance	4.3	1.0	1	5
Organizational identification	4.2	1.1	1	5
Employee loyalty	4.4	1.0	1	5
Job satisfaction	4.0	1.2	1	5
Turnover intention	1.5	1.0	0	3
Organizational citizenship behavior	3.5	1.0	1	5
Employee well-being	3.2	1.1	1	5
Work-life balance	3.0	1.2	1	5
Job stress	2.8	1.0	1	4
Organizational trust	4.0	1.0	1	5
Employee engagement	4.1	1.1	1	5
Job performance	4.3	1.0	1	5
Organizational identification	4.2	1.1	1	5
Employee loyalty	4.4	1.0	1	5

MNLVLDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLCSSSGGLNVTC SNANLKEI PRDL  
 PPETVLLYLDSNQITSIPNEIFKDLHQRLVNL SKNGIEFIDEHAFKGVAETLQTLDSLSDNR  
 IQSVHKNAFNNLKARARIANNPW HCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL  
 NAANDADLCNLPKKT TDYAMLVTMFGWFTMVISYV VYYVRQNQEDARRHLEYLKS LPSRQKK  
 ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

## FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCGAGATGCGAGGTGAGCAAGAGGATGCTGGCGGGG  
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCT  
GGGCTCAGTGCTGTGTCAGGCTCGGCCACGGGCTGCCGCCCGCTGCGAGTGCTCCGCCCAGG  
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG  
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTCGCCAG  
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCCGGCG  
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC  
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGAT  
CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG  
ACAATGACCTCGTCTACATCTCTCACC CGCCTT CAGCGGCCTCAACAGCCTGGAGCAGCTG  
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCCACCTGCACGGCCT  
CATCGTCTTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC  
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAC  
TGCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC  
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCTCAACCTCTCCTACAACCCCATCA  
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC  
GGGCAGCTGGCCGTGGTGGAGCCCTATGCCCTTCCGCGGCCCTCAACTACCTGCGCGTGCTCAA  
TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG  
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCCTGTGGGTGTTCCGG  
CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCCGAGTTTGTCCA  
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCAACTACTTCACCTGCCGCCGCG  
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACACGGTGCAGTTT  
GTGTGCCGGGCGGATGGCGACCCGCCGCCGCCATCCTCTGGCTCTCACCCCGAAAGCACCT  
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT  
ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGAC  
TCCATGCCCCGCCACCTGCATGTGCGCAGCTACTCGCCGACTGGCCCCATCAGCCCAACAA  
GACCTTCGCTTTCATCTCCAACAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG  
TGCCTTTCCTTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC  
CTGGGCGTCGTCTCTTCTGCCTGGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC  
AAAGCACAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG  
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGGCCGGGGCGGGGGGCAGGGACCCCCG  
GGCGGCCGGGCGAGGGGAAGGGGCTGGTGCACACCTGCTCACTCTCCAGTCTTCCCACCTC  
CTCCCTACCCTTCTACACACGTTCTCTTCTCCCTCCCGCTCCGTCCCTGCTGCCCCCG  
CCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCCAGACCTGGGGACCCCA  
CCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCA  
ATAATTCAATAAAAAAAGTTACGAACCTTCTCTGTAACCTGGGTTTCAATAATTATGGATTTT  
TATGAAAACCTTGAAATAATAAAAAAGAGAAAAAACTAAAAA

FIGURE 29

## **FIGURE 30**

MQVSKRMLAGGVSRMPSPLLACWQPILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFFNNLFLNLRTL  
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA  
FSGLSLEQLTLEKCNLTSSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH  
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSGNLETLILDSNPLA  
CDCRLLWVFRRRWRLNFNRRQOPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVPDGTLEVRYAQVQDNGTYL  
CIAANAGGND SMPAHLHVRSPDWPHQPNKTF AFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFCLVLLFLWSRGKGN TKH NIEIEYVPRKSDAGISSADAPRKFNMKMI

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 556-578

### **N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

### **Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

### **Tyrosine kinase phosphorylation site.**

amino acids 590-598

### **N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAAC  
ATCGTAGTCCACCCCCTCCCCATCCCCAGCCCCGGGGATTTCAGGCTCGCCAGCGCCCAGCC  
AGGGAGCCGGCCGGGAAGCGCGAATGGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGC  
TGTTCGCCTGCTGCTGGGCGCCCCGGCGGGGGCCAACCTCTCCCAGGACGACAGCCAGCCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGGTCAAGTGCCAAGTGAAAGATCA  
CGAGGACTCATCCCTGCAATGGTCTAACCCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA  
GAGCCCTTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT  
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTT  
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTGAGTCTTCTGGGAGCAAG  
CCTGCAGCCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT  
ACAGGAAGATCCCAATGGTAAACCTTCACTGTGACGAGCTCGGTGACATTCCAGGTTACCC  
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTTCCCTTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG  
CAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACCCAGTCCGGTGCCCT  
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCCTGCTG  
CTCATCATGCTCATCTTCCTTGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA  
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG  
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTTCATCTAGAGGCGCCTGCCCCACTTCCTGC  
GCCCCCAGGGGCCCTGTGGGGACTGCTGGGGCCGTACCAACCCGGACTTGTACAGAGCAA  
CCGCAGGGCCGCCCCCTCCCGCTTGCTCCCCAGCCCACCCACCCCCCTGTACAGAATGTCTGC  
TTTGGGTGCGGTTTTGTACTCGGTTTGGAATGGGGAGGGAGGAGGGCGGGGGGAGGGGAGGG  
TTGCCCTCAGCCCTTTCCTGCTGCTTCTGCTGCTTGGGTTATTATTATTTTGTAAACAATCC  
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA  
AACAAAAACA

TTTGGGTGCGGTTTTGTACTCGGTTTGGAATGGGGAGGGAGGAGGGCGGGGGGAGGGGAGGG

## **FIGURE 32**

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW  
SNPAQQTLTYFGEKRALRDNRILVTSTPHELSSISISNVALADEGEYTCSTFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLHCEGRGNPVPQQYLWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIIFLGHYLIRHKGTYLTAEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 331-352

### **N-glycosylation site.**

amino acids 25-29, 290-294

### **Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

### **N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18



General Information	
Project Name	...
Project Number	...
Project Manager	...
Project Sponsor	...
Project Start Date	...
Project End Date	...
Project Status	...
Project Description	...
Project Objectives	...
Project Scope	...
Project Budget	...
Project Resources	...
Project Risks	...
Project Issues	...
Project Deliverables	...
Project Milestones	...
Project Communication	...
Project Reporting	...
Project Documentation	...
Project Change Management	...
Project Quality Management	...
Project Risk Management	...
Project Stakeholder Management	...
Project Team Management	...
Project Procurement Management	...
Project Integration Management	...
Project Planning Management	...
Project Execution Management	...
Project Monitoring and Control Management	...
Project Closing Management	...

GGGGGTTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCTTTTCTTCTCCTTTCTCTGG  
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG  
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT  
GCTGGAGACGTCTCTTTGTTTTGCCGCTGAAACGTTACAGGGGACGTTTGCAAAGAGAAGA  
TCTGTTCCCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA  
AGTCTGCAGCGTTTCACTGCCCCGACTTCCAGTTTTACCATTATTTCTGCATGGCAATTC  
CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGG  
AAAACAATGGCTTGCATGAAATCGTTCCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGG  
CTGCACATCAACAACAACAAGATCAAGTCTTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATATAGACCCGGGGGCCTTCCAGG  
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC  
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC  
CTATGAGGAGGTCTTGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCTT  
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAAACATTCCCAAGAATGCC  
CTGATCGGCCGAGTGGTCTGCGAAGCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC  
CACCGAACAGGACTTGTGTCCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGGCGCCCCCTG  
CCCAAGAAGAGACCTTTGCTCCTGGAACCCCTGCCAACTCCTTTCAGACAAATGGGCAAGAG  
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCAGGCAACTGGCAGAT  
CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCCTTAGCTAACA  
GTTTACCCTGCCCTGGGGGCTGCAGCTGCGACCACATCCAGGGTTCGGGTTTAAAGATGAAC  
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCAGGA  
GCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA  
ACCTCATCTGTGTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACACTTTCAAG  
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA  
GAAATTTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA  
TCCTCCCGGGCACTTTCAATGCCATGCCCAAACCTGAGGATCCTCATTCTCAACAACAACCTG  
CTGAGGTCCCTGCCTGTGGACGTGTTTCGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCACAA  
CAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA  
TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCA  
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTTCTT  
TAGAAAGGATTTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
CGCCACAGTTAACTTCGCACAGTAAAAACAGCACTGGGTGCGGAGACCGGGACGCACTCC  
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCGGGACTGCTGCTGGT  
GTTTGTACCTCCGCCTTCACCGTGGTGGGCATGCTCGTGTTTATCCTGAGGAACCGAAAGC  
GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAAATCCCTACAGACAGTCTGT  
GACTCTTCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTG  
TGGCTCTCACTCGCTCTCAGACTAAGACCCCCAACCCCAATAGGGGAGGGGCAGAGGGAAGGCG  
ATACATCCTTCCCCACCGCAGGCACCCCGGGGGCTGGAGGGGCGTGTACCCAAATCCCGCG  
CCATCAGCCTGGATGGGCATAAGTAGATAAAATAACTGTGAGCTCGCACAAACCGAAAGGGCT  
GACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA  
GCCAGCTCGCTCTTTGCTGAGAGCCCCCTTTTGACAGAAAGCCCAGCACGACCCCTGCTGGAAG  
AACTGACAGTGCCTTCGCCCTCGGCCCGGGGCTGTGGGGTTGGATGCCGCGGTTCTATAC  
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTTCCCTGTGGATTAG  
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT  
TGTAATAAGTAACTTTGACTTCTGAC

## **FIGURE 34**

MLLWILLLETSLCFAAGNVTGDVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH  
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQ  
TFLGLDDLEYLQADFNLLRDIDPGAQDLNKLLEVLILNDNLISTLPANVFQYVPITHLDLRG  
NRLKTLPEYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ  
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGGLPTPFKTNGQEDHATPGSAPNGGK  
IPGNWQIKIRPTAAIATGSSRNKPLANSRPCPGGCSCDHIPGSGLMNCNNRNVSLLADLKP  
KLSNVQELFLRDNKKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQNLLEYLNVEYNAIQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL  
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGPNWECSTIVPFKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL  
VPGLLLVFVTSFTVVGMLVFILNRKRKRSDANSSASEINSLQTVCDSSYWHNGPYNADG  
AHRVYDCGSHSLSD

### **Signal sequence:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 618-638

### **N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

### **Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

### **N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCCCTGACCCCAGAATAACTCAGGGC  
TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTGCGGGCCTAAGGGAAACTGTTGGC  
CGCTGGGCCCCGCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTGCGTCTCTGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCGGGGCTCAG  
AGAATGAGGCCGGCGTTTCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCCGGCGG  
CGGCGAACACCCCACTGCCGACCGTGCTGGCTGCTCGGCCCTCGGGGGCCTGCTACAGCCTGC  
ACCACGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC  
AGCACCGTGCGTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCCAGG  
GCCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCCACT  
GCACCCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCCCGGCGGTCTC  
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGC  
GGTACTCCAGGCCACCGGTGGGGTGCAGCCCCGAGGCTGGAAGGAGATGCGATGCCACCTGC  
GCGCCAACGGCTACCTGTGCAAGTACCAGTTTGGAGGTCTTGTGTCCTGCGCCGCGCCCCGGG  
GCCGCCTCTAATTGAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGGACAGCTCCCGATCTCAGTTACTTGCA  
TCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTGCCCC  
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG  
CTTTGCCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCA  
GTGGGGAAGGACAGCCGACCCTTGGGGGGACCGGGGTGCCACCAGGCGCCCCGCCGCGCCACT  
GCAACCAGCCCCGTGCCGACAGACAATGGCCAATCAGGGTGCAGGAGAAGCTGGGAGAGAC  
ACCACTTGTCCCTGAACAAGACAATTGAGTAACATCTATTCTGAGATTCTTCGATGGGGAT  
CACAGAGCACGATGTCTACCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC  
CCATCAGGGAGCGTGATTTCCAAGTTTAAATTTCTACGACTTCCTCTGCCACTCCTCAGGCTTT  
CGACTCCTCCTCTGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCT  
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTACGAAAGCCCCCTCTTCCAGCCA  
AGGAAGGAGTCTATGGGCCCCGCGGGCCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC  
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTGGGGACTGTGATCTGCGGGACAGAG  
CAGAGGGTGCCTTGCTGGCGGAGTCCCCCTCTGGCTCTAGTGATGCATAGGGAAACAGGGGA  
CATGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACCTTAC  
TTGTGTAAGTGAACAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCCTTTACTCCACTGAG  
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCCTTTAGGA  
TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTCGGAGAA  
TTTGGAGAAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATATAATTTACA  
TTAAAAAATAATTTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTTCAGGCTAGGAGTAT  
ATTGTTTCGAAATCCCAGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

## **FIGURE 36**

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAEEACILRGGALS  
TVRAGAE LRAVLALLRAGPGPGGSKDLLFWVALERRRRSHCTLENEPLRGFSWLSSDPGGLE  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA  
ASNLSYRAPFQLHSAALDFSPGTEVSALCRGQLPISVTCTIADEIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTM TVLGLVKLCFHESPSSQPR  
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCLDRDRAEGALLAESPLGSSDA

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 399-418

### **N-glycosylation site.**

amino acids 189-193, 381-385

### **Glycosaminoglycan attachment site.**

amino acids 289-293

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

### **Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

### **N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## FIGURE 37

CGGACGCGTGGGATTGAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG  
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCTCCGCCCTGCCGGCCGCGTATC  
CCCCGGCTACCTGGGCGCGCCCGCGGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA  
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTGGGTGCGGA  
GGGGCGTGTGTGCCGGCGCGCGCGCCGTGGGGTGCAAACCCCGAGCGTCTACGCTGCCATGA  
GGGGCGCGAACGCCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG  
CAGCAGTCCCCAGAGAGACCTGTTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTTTCTGGAGTGTACCCTCCAAATAGCAAATGTACTTGGAATCA  
CAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTTCATAGACCTCGAGAGTGACAAC  
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTTGGCCG  
CTTCTGTGGCATTTCGCGCCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA  
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCGGCTCTTTTAAAC  
CCCCAACTGGCCAGACCGGGATTACCCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC  
CAAAGAATCAGCTTATAGAATTAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTTAAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACTTCTTATTCAGT  
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTCAGGCCAAAA  
AAACTGCCTACAACACAGAACAGCCTGTCACCACCACATTCCCTGTAACCACGGGTTTAA  
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGACGGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTTG  
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTCAGCAGGCGGG  
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC  
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAAACAGC  
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG  
TTAAAGTGAAGTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTT  
TCTCAGTAGAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG  
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTT  
TGCTGTGCTGTCAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCGGTGATAGGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAGCGTTTATTTATACATCTCTGTAAAAGGAT  
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATATTTATAGT  
GTTATTTGTTTCACCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGCGTTTTCTA  
AATCAATGCTTAATAAAATATTTTTAAAGGAAAAAAAAAAAA

TCCTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVPPNSKCTWK  
ITVPEGKVVVLNFRFIDLESNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSEARNELLI  
QFLSDLSLTADGFIGHYIFRPKKLPPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN  
YCSSDFVLACTVITTTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLR  
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

### **Signal sequence:**

amino acids 1-23

### **N-glycosylation site.**

amino acids 355-359

### **Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

### **Tyrosine kinase phosphorylation site.**

amino acids 199-208

### **N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

### **Cell attachment sequence.**

amino acids 149-152

FIGURE 38

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	21	55
Gender	0.5	0.5	0	1
Marital Status	0.6	0.5	0	1
Education	12.5	1.5	10	15
Income	3500	1500	1000	7000
Health	0.8	0.2	0	1
Smoking	0.3	0.5	0	1
Alcohol	0.2	0.4	0	1
Exercise	0.4	0.5	0	1
Stress	0.6	0.5	0	1
Sleep	0.7	0.3	0	1
Diet	0.5	0.5	0	1
Work	0.8	0.2	0	1
Family	0.6	0.5	0	1
Friends	0.7	0.4	0	1
Hobbies	0.5	0.5	0	1
Travel	0.4	0.5	0	1
Religion	0.6	0.5	0	1
Politics	0.5	0.5	0	1
Environment	0.7	0.4	0	1
Technology	0.6	0.5	0	1
Art	0.5	0.5	0	1
Music	0.6	0.5	0	1
Sports	0.7	0.4	0	1
Gardening	0.5	0.5	0	1
Reading	0.8	0.2	0	1
Writing	0.6	0.5	0	1
Volunteering	0.4	0.5	0	1
Charity	0.5	0.5	0	1
Philosophy	0.6	0.5	0	1
Science	0.7	0.4	0	1
History	0.5	0.5	0	1
Geography	0.6	0.5	0	1
Language	0.7	0.4	0	1
Mathematics	0.5	0.5	0	1
Physics	0.6	0.5	0	1
Chemistry	0.7	0.4	0	1
Biology	0.5	0.5	0	1
Medicine	0.6	0.5	0	1
Law	0.7	0.4	0	1
Business	0.5	0.5	0	1
Engineering	0.6	0.5	0	1
Architecture	0.7	0.4	0	1
Design	0.5	0.5	0	1
Art History	0.6	0.5	0	1
Music History	0.7	0.4	0	1
Sports History	0.5	0.5	0	1
Gardening History	0.6	0.5	0	1
Reading History	0.7	0.4	0	1
Writing History	0.5	0.5	0	1
Volunteering History	0.6	0.5	0	1
Charity History	0.7	0.4	0	1
Philosophy History	0.5	0.5	0	1
Science History	0.6	0.5	0	1
History History	0.7	0.4	0	1
Geography History	0.5	0.5	0	1
Language History	0.6	0.5	0	1
Mathematics History	0.7	0.4	0	1
Physics History	0.5	0.5	0	1
Chemistry History	0.6	0.5	0	1
Biology History	0.7	0.4	0	1
Medicine History	0.5	0.5	0	1
Law History	0.6	0.5	0	1
Business History	0.7	0.4	0	1
Engineering History	0.5	0.5	0	1
Architecture History	0.6	0.5	0	1
Design History	0.7	0.4	0	1
Art History History	0.5	0.5	0	1
Music History History	0.6	0.5	0	1
Sports History History	0.7	0.4	0	1
Gardening History History	0.5	0.5	0	1
Reading History History	0.6	0.5	0	1
Writing History History	0.7	0.4	0	1
Volunteering History History	0.5	0.5	0	1
Charity History History	0.6	0.5	0	1
Philosophy History History	0.7	0.4	0	1
Science History History	0.5	0.5	0	1
History History History	0.6	0.5	0	1
Geography History History	0.7	0.4	0	1
Language History History	0.5	0.5	0	1
Mathematics History History	0.6	0.5	0	1
Physics History History	0.7	0.4	0	1
Chemistry History History	0.5	0.5	0	1
Biology History History	0.6	0.5	0	1
Medicine History History	0.7	0.4	0	1
Law History History	0.			

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	21	55
Gender	0.5	0.5	0	1
Marital Status	0.6	0.5	0	1
Education	12.5	1.5	10	15
Income	3500	1500	1000	7000
Health	0.8	0.2	0	1
Smoking	0.3	0.5	0	1
Alcohol	0.2	0.4	0	1
Exercise	0.4	0.5	0	1
Stress	0.6	0.5	0	1
Sleep	0.7	0.3	0	1
Diet	0.5	0.5	0	1
Work	0.8	0.2	0	1
Family	0.6	0.5	0	1
Friends	0.7	0.4	0	1
Hobbies	0.5	0.5	0	1
Travel	0.4	0.5	0	1
Religion	0.6	0.5	0	1
Politics	0.5	0.5	0	1
Environment	0.7	0.4	0	1
Technology	0.6	0.5	0	1
Art	0.5	0.5	0	1
Music	0.6	0.5	0	1
Sports	0.7	0.4	0	1
Gardening	0.5	0.5	0	1
Reading	0.8	0.2	0	1
Writing	0.6	0.5	0	1
Volunteering	0.4	0.5	0	1
Charity	0.5	0.5	0	1
Philanthropy	0.6	0.5	0	1
Leadership	0.7	0.4	0	1
Teamwork	0.8	0.2	0	1
Communication	0.9	0.1	0	1
Problem Solving	0.8	0.2	0	1
Decision Making	0.7	0.3	0	1
Time Management	0.6	0.4	0	1
Organization	0.7	0.4	0	1
Planning	0.8	0.2	0	1
Execution	0.9	0.1	0	1
Monitoring	0.8	0.2	0	1
Evaluation	0.7	0.3	0	1
Reflection	0.6	0.4	0	1
Learning	0.9	0.1	0	1
Growth	0.8	0.2	0	1
Change	0.7	0.3	0	1
Adaptation	0.8	0.2	0	1
Resilience	0.9	0.1	0	1
Optimism	0.8	0.2	0	1
Positivity	0.9	0.1	0	1
Gratitude	0.7	0.3	0	1
Forgiveness	0.6	0.4	0	1
Patience	0.7	0.4	0	1
Kindness	0.8	0.2	0	1
Compassion	0.9	0.1	0	1
Empathy	0.8	0.2	0	1
Understanding	0.9	0.1	0	1
Acceptance	0.7	0.3	0	1
Openness	0.8	0.2	0	1
Curiosity	0.9	0.1	0	1
Imagination	0.7	0.3	0	1
Creativity	0.8	0.2	0	1
Innovation	0.9	0.1	0	1
Entrepreneurship	0.7	0.3	0	1
Leadership	0.8	0.2	0	1
Teamwork	0.9	0.1	0	1
Communication	0.8	0.2	0	1
Problem Solving	0.9	0.1	0	1
Decision Making	0.7	0.3	0	1
Time Management	0.8	0.2	0	1
Organization	0.9	0.1	0	1
Planning	0.7	0.3	0	1
Execution	0.8	0.2	0	1
Monitoring	0.9	0.1	0	1
Evaluation	0.7	0.3	0	1
Reflection	0.8	0.2	0	1
Learning	0.9	0.1	0	1
Growth	0.7	0.3	0	1
Change	0.8	0.2	0	1
Adaptation	0.9	0.1	0	1
Resilience	0.7	0.3	0	1
Optimism	0.8	0.2	0	1
Positivity	0.9	0.1	0	1
Gratitude	0.7	0.3	0	1
Forgiveness	0.8	0.2	0	1
Patience	0.9	0.1	0	1
Kindness	0.7	0.3	0	1
Compassion</				

## **FIGURE 40**

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLPQSPPPQSSPPPPQHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDCQAG  
YGGEACGQCGLGYFEARNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG  
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

### **Signal sequence:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 372-395

### **N-glycosylation site.**

amino acids 79-83, 205-209

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

### **Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

### **N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

### **EGF-like domain cysteine pattern signature.**

amino acids 181-193



## **FIGURE 41**

TGAGACCCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCCCTGGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT  
GCCCACCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGGCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTTTCAGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTCTTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTCGG  
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCCAGG  
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGGCGGCTGTCCCCGCGCAGCGCCCCGGGCC  
CGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA  
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTGGTGCAGAGG  
GAGCATCTGGGCCCCGCTGGCGTCCGGCGCCCAAGCTGGTCCGCTTTGCCTCGCAGGGGGC  
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTGGACCTTGGGGACTATGGAG  
CTCAGGGCGACTGTGACCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCCGGGCTT  
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCCTTCAAGTGGC  
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCAAGGAGGCTCCAGCCATAGCGCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTTCGAGGGTACCAGGAGAGCTG  
GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT  
CCTCTGACAAGTTACCTCACCTAATTTTTTGCTTCTCAGGAATGAGAATCTTTGGCCACTGGA  
GAGCCCTTGCTCAGTTTTCTCTATTCTTATTATTCACTGCACTATATTCTAAGCACTTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCAATTGTTTACTTGTCTGTCTCAC  
TGGATCTGGGCTAAAGTCCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAACATGAATAAAACACATTTTATTCT  
AAAA

“39440560”

## **FIGURE 42**

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFSQSFRVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP  
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF  
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTCRQPPEALAFKWPF  
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKSCASDGALVPRRLQP

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 158-162

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

### **N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

### **Amidation site.**

amino acids 74-78

### **TGF-beta family signature.**

amino acids 282-298

[illegible]

GTCTGTTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTGTCAGTGGCCTGATCGCGAATCGGGGACAAA  
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG  
CATTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCTTGAGAATAATCCT  
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA  
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG  
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTCTGCCACCATTGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT  
GGGATAGTGATGCCTACGAATCCCAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCTCT  
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCTGTGAGCCTCTGATACTGGAGAATACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT  
GTGGAGCGGAATGTGGGGGTGTCGTGGCAGCCGTCCTTGTAACCCTGATTCTCCTGGGAAT  
CTTGTTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTCTGGTGTTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCTTACT  
CAGGTGCTACCGGACTCTGGCCCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTC  
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC  
ATCCTCCTTCATGCCCTCCCTCCCTTTCTTACCCTGCTGAGTGGCCTGGAACTTGTTTAAA  
GTGTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGCAAAAATGGCGGGGGTTCGAGGAATCTGCACTCAACTGCCCACCTGGC  
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGTTCTGGGCTCTTTCCTTGTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG  
TGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG  
CCACTGGGATCCCTCTGCCCTGTCCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT  
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG  
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTG  
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGCGGAGTTGCGGATCAGCCTGACCA  
ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACCTCCAGCTCAAAAAAAAAAAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLS CAYSGFSSPRVEW  
KFDQGD TTRLVCYNNKITASYEDRV TFLPTGITFKSV TREDTGTYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNS  
SYVLNPTTGELVFDP L S ASDTGEYSCEARNGYGT PMTSNAVRMEAVERNVGVIVA AVLVTLI  
LLGILVFGIWFAYS RGHFDR TKKGTS SKKVIYSQPSARSEGEFKQTSSFLV

### **Signal sequence:**

amino acids 1-27

### **Transmembrane domain:**

amino acids 238-255

### **N-glycosylation site.**

amino acids 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

### **Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

### **N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## **FIGURE 45**

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCGCGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCGCGAGGCCCCAGCTCAG  
GCTCGTGCCACCCACCAAGTTCCAGTGCCGCACCAAGTGGCTTATGCGTGCCCCCTCACCTGG  
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCCACCGCCCCCTGGCCTCCCCTGCCCTGCACCGGCGTCA  
GTGACTGCTCTGGGGGAACTGACAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCA  
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA  
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG  
GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCC  
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTCGGGAATGCCACATCCTC  
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC  
TCAGTGCAAGCCTGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGC  
CTCCGCCCCTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGAC  
CTCGCTGCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA  
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAG  
GGGCTGGCCCCAGGCAGCTCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 45

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCDRDLDCSDGSDEEEECRIEPCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL  
RNCSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVT  
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSP TAYGVIAAAVLSASLVTATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

### **Signal sequence:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 230-246

### **N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

### **Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

### **N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

### **Leucine zipper pattern.**

amino acids 17-39

## FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTGCGGCACAGATGCGG  
GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA  
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT  
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGA  
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA  
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTGATGAAGGATTCAAGATCCGG  
TACCCCGACCTACACAATATGGTTTCATTATGTCGCGATGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC  
TCCAGACCTCCTTCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCTCGGATTTAAACTT  
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCACCCCGGTG  
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGTCT  
GCCACCCGCGGCCTTGTGAGCGCTACAACCACGGAACGTGTGGTGGAGTTTTACTGCGATCCT  
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTC  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCTCCTGA  
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGCTGCTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCTCCCCGGAG  
TTCCAGCAGTGACCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATG  
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCCTTAGGCCCGGTACATGGCCTCTGTGGGCCAG  
GGCTGCCCCCTTACCCGTGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA  
CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA  
GTCTGTATTACCTCCCAGGTGCCAAGAGAGCACCCACCTGCTTCGGACAACCCTGACATA  
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATCATGCCCACTGGGT  
GTTGTTCTTAAGAAACTGATTGATTAAAAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAA  
ATACATGTTGATCTGTGGAGTTGATTCTTTCTCTTCTTGGTTTTAGACAAATGTAAACAA  
AGCTCTGATCCTTAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC  
CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAAGNAAAAAA

FIGURE 47

## **FIGURE 48**

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFAHFPPRGPPRSSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDTGPGESETCDS  
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVFLRN

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 325-344

### **N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

### **Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

### **N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405



## FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCCCCGCTCCCGTGCGGTCCGTCGGTGGCCTAGAGA  
TGCTGCTGCCGCGGTTGCAGTTGTGCGGCACGCCTCTGCCCGCCAGCCCGCTCCACCGCCGT  
AGCGCCCGAGTGTCTGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG  
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC  
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTTA  
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAA  
AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT  
CACAAATTTAGGAACTGGTATGTGGATGAGCCGTCTTGCGGCAGCGAGGTCTGCGTGGTCATG  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGA  
CCGGTGCAACATGAAGAACAATTTCAATTTGCAAATATTCTGATGAGAAACCAGCAGTTCCTT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG  
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT  
CCTAATCCCCAGCATTCCCCCTTCTCCTCCTCCTTGTGGTCACCACAGTTGTATGTTGGGTTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC  
TGGCCCTCTCCTCACCAGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTT  
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA  
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGAGAGTGGATTTGTGACCAATGACATTTATGA  
GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG  
GTTATTAGGACATATAAAAACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC  
CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT  
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTTGGCTGTATCCTTTAT  
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCAGGTCTGGCACATAGTA  
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG  
GCAGTGATAAAGATGGGCTGTGGAGCTTGGAACCACCTCTGTTTTCTTGCTCTATACAG  
CAGCACATATTATCATACAGACAGAAAATCCAGAATCTTTTCAAAGCCCACATATGGTAGCACAG  
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTTCAAAGAATAAAATCAAATAAAGA  
GCAGGAAAAAAAAA

## **FIGURE 50**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGGTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSI ESEDEQKLI EKFIENLLPSDGDFWIGLRRREEKQSNSTACQDL  
YAWTDGSISQFRNWWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY  
SDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPSIPLLLLLLV  
VTTVVCWWVICRKRKREQPD PSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL  
KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTILSVESGFVTNDIYEFSPDQMGRSKES  
GWVENEIYGY

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 117-121, 312-316

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

### **Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

### **N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
Male	55.2 (10.5)
Female	56.8 (11.2)
Marital status	
Married	78.5%
Single	21.5%
Education level	
High school or above	65.2%
Below high school	34.8%
Occupation	
White collar	45.1%
Blue collar	54.9%
Income (USD/month)	
< 1000	12.3%
1000-2000	35.7%
2000-3000	28.9%
> 3000	23.1%
Health insurance	
Yes	89.4%
No	10.6%
Comorbidities	
Hypertension	42.1%
Diabetes	18.5%
Cholesterol	31.2%
Smoking status	
Current smoker	15.3%
Former smoker	22.7%
Non-smoker	62.0%

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT  
GTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAACCTC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT  
GCAGCAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC  
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTTCGTTCCACTAACATTTTTTCGGAATCTG  
GAGTCCACCCGTTGTTTGGCTGGCTGGGCTTTTTCCAGTGTCAGAAAGAAGGACCCATCATCAT  
CCCACTGATGAAGCAGATTCAGAAGTCTTGTATCCCAACTACCAAAGCTGCTGGAGCCTGA  
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG  
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT  
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG  
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG  
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTTGACCACAAATGGCCACCGTTTGCT  
GTTGACCTGACCATGGAACCTTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA  
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCCGCTGGACATGT  
TCTTGAATGCCATGTCACTTTATACCTTAAGCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAAGTGCCTTTTATACAATG

## **FIGURE 52**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQRTGRRTASLQPGISEDLLKKVKDRMGIDSSDKVD  
FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPPFLHILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTLGIFDHKWPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

### **Signal sequence:**

amino acids 1-23

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

### **Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

### **Tyrosine kinase phosphorylation site.**

amino acids 280-288

### **N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

### **Amidation site.**

amino acids 216-220

### **Leucine zipper pattern.**

amino acids 10-32

### **Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

FIGURE 52

## FIGURE 53

CTCCTCTTAACATACTTGACAGCTAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT  
TAAATTTTACAGCTCATCACCTTCACCTGCCTTGGTCAATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG  
ATTGTTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCAGAGAGCTCTTTCTCCCCA  
GTCCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA  
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAAGGTGG  
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTGCTGCTCAGGACGAGAAGCAACCCTTCA  
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCTG  
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACTGGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA  
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTTCGTTGCTCAGGGGAGGAG  
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTACGACTGCACCCACCAGGAAGA  
TGTGGCTGTGCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT  
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCCCTGATTCTCAGGCCTTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACCTACATCA  
CCACCTTTTCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT  
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA  
CACCATTTGTCCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTTTAAAGGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTTATTTACAATAATAAAGATAGCAC  
TATGTGTTCAAA

## **FIGURE 54**

MALLFSLILAICTRPGFLASPSGVRLVGGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC  
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC  
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCTGWSLRAAKVVCRQLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMSSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCSGRLEVLHKGWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

### **Signal sequence:**

amino acids 1-15

### **Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

### **N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

### **Amidation site.**

amino acids 196-200

### **Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCCCTGCTGTTCCGGCTGCCTGGG  
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT  
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA  
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC  
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA  
TGTGGACAAGAGGGTCATGGAGACAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCCTTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA  
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTTGCTGCTGTGGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA  
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC  
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC  
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTTGTCTCACAAGTGGG  
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA  
AGCTTCTTCCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACT  
AAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTAC

## **FIGURE 56**

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA  
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL  
VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQGKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 104-120, 278-292

### **N-glycosylation site.**

amino acids 228-232

### **Glycosaminoglycan attachment site.**

amino acids 47-51

### **Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

### **Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

### **N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

### **Amidation site.**

amino acids 265-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17



## FIGURE 57

CCCACGCGTCCGCTGGTGTTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA  
AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC  
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTTAA  
GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA  
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG  
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTTACATACCTTTGT  
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGACATTTCTGGACTACAAA  
GGCATTTCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCAGTGTGGCTTCGGCAG  
CTGGACATGTCTCGGTCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA  
TTTCATAAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG  
TCTGTGTCCTAATTTCTGTAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA  
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG  
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCCTGAGCGTTT  
CCTGGCAGTTTTTAAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCAATAAGCACCTAGTTTTCTGAAAACCTGATTTACCAGGTTTAGGTTGATGTCATCTA  
ATAGTGCCAGAATTTTAATGTTTGAACCTTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA  
TCATTTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT  
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA  
CCAAAATGACTTTTATTAATAAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA  
AATTTGTACCATAACCGTTTATTTAACATATATTTTTATTTTTGATTGCACTTAAATTTTGT  
ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA  
TGAAGGACTATATCTAGTGGTATTTCACAATGAATATCATGAACTCTCAATGGGTAGGTTTC  
ATCCTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT  
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG  
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA  
AA  
AA

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## **FIGURE 58**

MKFLLDILLLLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

### **Signal sequence:**

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

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Table 1. Demographic characteristics of the study population	
Age (years)	65.0 ± 1.5
Gender	
Male	50.0
Female	50.0
Education (years)	12.0 ± 1.0
Marital status	
Married	70.0
Single	30.0
Occupation	
Retired	80.0
Unemployed	20.0
Income (USD/month)	1,200.0 ± 200.0
Health status	
Good	60.0
Fair	40.0
Poor	10.0
Comorbidities	
Hypertension	45.0
Diabetes	35.0
Cholesterol	25.0
Arthritis	15.0
Depression	10.0
Medication use	
Yes	75.0
No	25.0
Quality of life (SF-36)	50.0 ± 10.0
Physical function	40.0 ± 8.0
Bodily pain	55.0 ± 12.0
General health	60.0 ± 15.0
Energy/fatigue	45.0 ± 10.0
Social functioning	50.0 ± 12.0
Emotional well-being	55.0 ± 10.0
Role limitations	40.0 ± 10.0
Healthcare utilization	
Primary care visits (per year)	5.0 ± 2.0
Specialty care visits (per year)	2.0 ± 1.0
Hospitalizations (per year)	1.0 ± 0.5
Emergency department visits (per year)	0.5 ± 0.3
Medication adherence (%)	70.0 ± 15.0
Health insurance status	
Medicaid	60.0
Medicare	40.0
Private	10.0
Health literacy score	6.0 ± 1.0
Health knowledge score	7.0 ± 1.0
Health beliefs score	8.0 ± 1.0
Health motivation score	9.0 ± 1.0
Health self-efficacy score	10.0 ± 1.0
Health decision-making score	11.0 ± 1.0
Health communication score	12.0 ± 1.0
Health management score	13.0 ± 1.0
Health monitoring score	14.0 ± 1.0
Health evaluation score	15.0 ± 1.0
Health improvement score	16.0 ± 1.0
Health maintenance score	17.0 ± 1.0
Health protection score	18.0 ± 1.0
Health promotion score	19.0 ± 1.0
Health prevention score	20.0 ± 1.0
Health recovery score	21.0 ± 1.0
Health rehabilitation score	22.0 ± 1.0
Health restoration score	23.0 ± 1.0
Health repair score	24.0 ± 1.0
Health replacement score	25.0 ± 1.0
Health restoration score	26.0 ± 1.0
Health repair score	27.0 ± 1.0
Health replacement score	28.0 ± 1.0
Health restoration score	29.0 ± 1.0
Health repair score	30.0 ± 1.0
Health replacement score	31.0 ± 1.0
Health restoration score	32.0 ± 1.0
Health repair score	33.0 ± 1.0
Health replacement score	34.0 ± 1.0
Health restoration score	35.0 ± 1.0
Health repair score	36.0 ± 1.0
Health replacement score	37.0 ± 1.0
Health restoration score	38.0 ± 1.0
Health repair score	39.0 ± 1.0
Health replacement score	40.0 ± 1.0
Health restoration score	41.0 ± 1.0
Health repair score	42.0 ± 1.0
Health replacement score	43.0 ± 1.0
Health restoration score	44.0 ± 1.0
Health repair score	45.0 ± 1.0
Health replacement score	46.0 ± 1.0
Health restoration score	47.0 ± 1.0
Health repair score	48.0 ± 1.0
Health replacement score	49.0 ± 1.0
Health restoration score	50.0 ± 1.0
Health repair score	51.0 ± 1.0
Health replacement score	52.0 ± 1.0
Health restoration score	53.0 ± 1.0
Health repair score	54.0 ± 1.0
Health replacement score	55.0 ± 1.0
Health restoration score	56.0 ± 1.0
Health repair score	57.0 ± 1.0
Health replacement score	58.0 ± 1.0
Health restoration score	59.0 ± 1.0
Health repair score	60.0 ± 1.0
Health replacement score	61.0 ± 1.0
Health restoration score	62.0 ± 1.0
Health repair score	63.0 ± 1.0
Health replacement score	64.0 ± 1.0
Health restoration score	65.0 ± 1.0
Health repair score	66.0 ± 1.0
Health replacement score	67.0 ± 1.0
Health restoration score	68.0 ± 1.0
Health repair score	69.0 ± 1.0
Health replacement score	70.0 ± 1.0
Health restoration score	71.0 ± 1.0
Health repair score	72.0 ± 1.0
Health replacement score	73.0 ± 1.0
Health restoration score	74.0 ± 1.0
Health repair score	75.0 ± 1.0
Health replacement score	76.0 ± 1.0
Health restoration score	77.0 ± 1.0
Health repair score	78.0 ± 1.0
Health replacement score	79.0 ± 1.0
Health restoration score	80.0 ± 1.0
Health repair score	81.0 ± 1.0
Health replacement score	82.0 ± 1.0
Health restoration score	83.0 ± 1.0
Health repair score	84.0 ± 1.0
Health replacement score	85.0 ± 1.0
Health restoration score	86.0 ± 1.0
Health repair score	87.0 ± 1.0
Health replacement score	88.0 ± 1.0
Health restoration score	89.0 ± 1.0
Health repair score	90.0 ± 1.0
Health replacement score	91.0 ± 1.0
Health restoration score	92.0 ± 1.0
Health repair score	93.0 ± 1.0
Health replacement score	94.0 ± 1.0
Health restoration score	95.0 ± 1.0
Health repair score	96.0 ± 1.0
Health replacement score	97.0 ± 1.0
Health restoration score	98.0 ± 1.0
Health repair score	99.

CCAACGCGTCCGCGGACGCGTGGGTGCGACTAGTTCTAGATCGCGAGCGGCCGCCCGCGGCTC  
 AGGGAGGAGCACCGACTGCGCCGCACCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG  
 TTTTCGCTGGTCTGTGTTGATGCCTGGCCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT  
 GTTTCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC  
 TGGGAAGATCCAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCCAGGACTGAACATGA  
 AGAGTTATGCCGGCTTCCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTC  
 TCCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG  
 AGGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCCTTATGTTGTCACAAGTAACATGA  
 CTTTGCCTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCA  
 GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT  
 AGCACGGGATTTATACAGTGCATAATTGAGTTTTTCCAGATATTTCTGAATATAAAAATA  
 ATGACTTTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC  
 ATCCATTCCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA  
 TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCT  
 GTTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC  
 AGGAAGCAGAACTGGTTTGAGGCCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC  
 AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTTGCGGT  
 GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTTGTCACTCCCAGAGGTGAGACAA  
 GCCATCCACGTGGGGAATCAGACTTTTAATGATGGAACCTATAGTTGAAAAGTACTTGCGAGA  
 AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA  
 TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC  
 ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAGTTTGGAAGATCTTTAA  
 ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC  
 GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA  
 TTCATTTATGAAAAGGATGGGATCCTTATGTTGGATTAACCTACCTTCCCAAAGAGAACAT  
 CAGAGGTTTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAA  
 TTATCTTTTCATATCTGCAAGATTTTTTTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGC  
 TTTTGTTTTTTGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA  
 TTATTTAACTTAAAGGATGAAGGATGATGGATGTGACACTGAGACAAGATGTATAAAATGA  
 AATTTTAGGGTCTTGGAATAGGAAGTTTAAATTTCTTCTAAGAGTAAGTGAAAAGTCAGTTG  
 TAACAAACAAAGCTGTAACATCTTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGT  
 GTTTGGAATATTATTGGATAAGAATAGCTCAATTATCCCAAATAAATGGATGAAGCTATAA  
 TAGTTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAATA  
 AAAATATTATATATAAAAGTAAAAA

## **FIGURE 60**

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRELSL  
VGPFPGLNMKSYAGFLTVNKTYSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTSNMTLRDRDFPWTTTSLMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQT  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHSLNPVREVKINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNVGT  
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT  
EIMNNYKVLIIYNGQLDIIVAAALTERSLMGMDWKGSQYKKAEEKVWKIFKSDSEVAGYIRQ  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

### **Signal sequence:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

### **Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

### **Tyrosine kinase phosphorylation site.**

amino acids 423-432

### **N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

### **Serine carboxypeptidases, serine active site.**

amino acids 200-208

### **Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

TDCT 20 20440660

1. 1990-1991 2. 1991-1992 3. 1992-1993 4. 1993-1994 5. 1994-1995 6. 1995-1996 7. 1996-1997 8. 1997-1998 9. 1998-1999 10. 1999-2000 11. 2000-2001 12. 2001-2002 13. 2002-2003 14. 2003-2004 15. 2004-2005 16. 2005-2006 17. 2006-2007 18. 2007-2008 19. 2008-2009 20. 2009-2010 21. 2010-2011 22. 2011-2012 23. 2012-2013 24. 2013-2014 25. 2014-2015 26. 2015-2016 27. 2016-2017 28. 2017-2018 29. 2018-2019 30. 2019-2020 31. 2020-2021 32. 2021-2022 33. 2022-2023 34. 2023-2024 35. 2024-2025 36. 2025-2026 37. 2026-2027 38. 2027-2028 39. 2028-2029 40. 2029-2030 41. 2030-2031 42. 2031-2032 43. 2032-2033 44. 2033-2034 45. 2034-2035 46. 2035-2036 47. 2036-2037 48. 2037-2038 49. 2038-2039 50. 2039-2040 51. 2040-2041 52. 2041-2042 53. 2042-2043 54. 2043-2044 55. 2044-2045 56. 2045-2046 57. 2046-2047 58. 2047-2048 59. 2048-2049 60. 2049-2050 61. 2050-2051 62. 2051-2052 63. 2052-2053 64. 2053-2054 65. 2054-2055 66. 2055-2056 67. 2056-2057 68. 2057-2058 69. 2058-2059 70. 2059-2060 71. 2060-2061 72. 2061-2062 73. 2062-2063 74. 2063-2064 75. 2064-2065 76. 2065-2066 77. 2066-2067 78. 2067-2068 79. 2068-2069 80. 2069-2070 81. 2070-2071 82. 2071-2072 83. 2072-2073 84. 2073-2074 85. 2074-2075 86. 2075-2076 87. 2076-2077 88. 2077-2078 89. 2078-2079 90. 2079-2080 91. 2080-2081 92. 2081-2082 93. 2082-2083 94. 2083-2084 95. 2084-2085 96. 2085-2086 97. 2086-2087 98. 2087-2088 99. 2088-2089 100. 2089-2090 101. 2090-2091 102. 2091-2092 103. 2092-2093 104. 2093-2094 105. 2094-2095 106. 2095-2096 107. 2096-2097 108. 2097-2098 109. 2098-2099 110. 2099-2100 111. 2100-2101 112. 2101-2102 113. 2102-2103 114. 2103-2104 115. 2104-2105 116. 2105-2106 117. 2106-2107 118. 2107-2108 119. 2108-2109 120. 2109-2110 121. 2110-2111 122. 2111-2112 123. 2112-2113 124. 2113-2114 125. 2114-2115 126. 2115-2116 127. 2116-2117 128. 2117-2118 129. 2118-2119 130. 2119-2120 131. 2120-2121 132. 2121-2122 133. 2122-2123 134. 2123-2124 135. 2124-2125 136. 2125-2126 137. 2126-2127 138. 2127-2128 139. 2128-2129 140. 2129-2130 141. 2130-2131 142. 2131-2132 143. 2132-2133 144. 2133-2134 145. 2134-2135 146. 2135-2136 147. 2136-2137 148. 2137-2138 149. 2138-2139 150. 2139-2140 151. 2140-2141 152. 2141-2142 153. 2142-2143 154. 2143-2144 155. 2144-2145 156. 2145-2146 157. 2146-2147 158. 2147-2148 159. 2148-2149 160. 2149-2150 161. 2150-2151 162. 2151-2152 163. 2152-2153 164. 2153-2154 165. 2154-2155 166. 2155-2156 167. 2156-2157 168. 2157-2158 169. 2158-2159 170. 2159-2160 171. 2160-2161 172. 2161-2162 173. 2162-2163 174. 2163-2164 175. 2164-2165 176. 2165-2166 177. 2166-2167 178. 2167-2168 179. 2168-2169 180. 2169-2170 181. 2170-2171 182. 2171-2172 183. 2172-2173 184. 2173-2174 185. 2174-2175 186. 2175-2176 187. 2176-2177 188. 2177-2178 189. 2178-2179 190. 2179-2180 191. 2180-2181 192. 2181-2182 193. 2182-2183 194. 2183-2184 195. 2184-2185 196. 2185-2186 197. 2186-2187 198. 2187-2188 199. 2188-2189 200. 2189-2190 201. 2190-2191 202. 2191-2192 203. 2192-2193 204. 2193-2194 205. 2194-2195 206. 2195-2196 207. 2196-2197 208. 2197-2198 209. 2198-2199 210. 2199-2200 211. 2200-2201 212. 2201-2202 213. 2202-2203 214. 2203-2204 215. 2204-2205 216. 2205-2206 217. 2206-2207 218. 2207-2208 219. 2208-2209 220. 2209-2210 221.	
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CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACAT  
TTTTCCCTTTTCTAACAAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG  
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGGAGGGCCTGCCTAACAAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCCTAATATCAAATTGACTGGCTGGC  
TGAAC'TTCAACAGCCTTTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA  
TAGAGATGCTTTGTAAAATAAAATTTTAAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAAGAGGGAGAAAAGTATGTTAAAAATA  
GAAAAACCAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCTGGGTC  
AGGCCAGCCTCTTTGCTCCTCCCGAAATATTTTTTGGTCTGACCACTCTGCCTTGTGTTTT  
GCAGAATCATGTGAGGGCCAACCCGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT  
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG  
ACAGCCGCTCTGTGGTCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCCCCAGCAGCCGGC  
ATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCCTTGACCGT  
CCACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG  
CCCCTCATCGTGACGCCCTGCAGCGAAGTGCTCACCCCTACCAACAATGTCAACAAGCTGCT  
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCA  
AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCCAAGAAGGAGCACTAC  
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA  
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCTGTCCA  
GCCGGAAGCTGCCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT  
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACAT  
CTTCTACATCTACGGCTTTGCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA  
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGCGG  
CTCTGCAAGGATGACCCCAAGTTCCACTCATACTGTCCCTGCCCTTCGGCTGCACCCGGGC  
CGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC  
AGGCC'TTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAG  
CAGTATCACCACCCGCCCGATGACTCTGCCCTGTGTGCCCTTCCCTATCCGGGCCATCAACTT  
GCAGATCAAGGAGCGCCTGCAGTCTGTCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC  
TGCTGGGGAAGGACGTCCAGTGCACGAAGGCGCCTGTCCCCATCGATGATAACTTCTGTGGA  
CTGGACATCAACCAGCCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCCTGTACACCAC  
CAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTTG  
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC  
ATTACCTCCTCAGCAAAGAGTCCCTCTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAG  
GCAACTTTATTTTTCTTGGGGAAACAAAGGTGGAATGGGGAGGTAAGAAGGGGTAAATTTTTGTG  
ACTTAGCTTCTAGCTACTTCCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA  
TTTCAATATTTCCCAAACCTTTAAGAAAAAACTTTAAGAAGGTACATCTGCAAAAGCAAA

## **FIGURE 62**

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP  
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV  
YKLTGNLTIQVAHKTGPEEDNKSRYPPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLACGSL  
YQGVCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY  
FPTLSSRKLPRDPESAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYG FASGGFVYFL  
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPRAINLQIKERLQSCYQGEGN  
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVFVGTKSGKLKKVRVYEFRC SNAIHLLSKESLLEGSYWWRFNRYRQLYFLGEQR

### **Signal sequence:**

amino acids 1-32

### **Transmembrane domain:**

amino acids 71-87

### **N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

### **Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

### **N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## FIGURE 63

AGGCTCCCCGCGCGCGGCTGAGTGCGGACTGGAGTGGGAACCCGGGTCCCCGCGCTTAGAGAACACGCGATGACCA  
CGTGGAGCCTCCGGCGGAGGCCGCGCCGACGCTGGGACTCCTGCTGCTGGTCTGCTTTGGGCTTCTGGTGCTCC  
GCAGGCTGGACTGGAGCACCTTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA  
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTTCGGGGGCTCCATCCACTATTTCCGTGTGCCAGGGAGTACT  
GGAGGGACCGCCTGCTGAAGATGAAGGCCTGTGGCTTGAACACCCCTCACCACCTATGTTCCGTGGAACCTGCATG  
AGCCAGAAAGAGGCAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCCTTCGTCTGATGGCCGACAGATCG  
GGCTGTGGGTGATTCTGCGTCCAGGCCCCCTACATCTGCAGTGAGATGGACCTCGGGGGCTTGCCAGCTGGCTAC  
TCCAAGACCTTGGCATGAGGCTGAGGACAACCTTACAAGGGCTTACCAGAAGCAGTGGACCTTTATTTTGACCACC  
TGATGTCCAGGGTGGTGCCACTCCAGTACAAGCGTGGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATG  
GTTCTTATAATAAAGACCCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGGAACCTGC  
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTCTTGCCACCATCAACTTGCAGT  
CAACACACGAGCTGCAGCTACTGACCACCTTTCTCTTCAACGTCCAGGGGACTCAGCCCAAGATGGTGATGGAGT  
ACTGGACGGGGTGGTTTGAATCGTGGGGAGGCCCTCACATATCTTGGATTCTTCTGAGGTTTTGAAAACCGTGT  
CTGCCATTGTGGACGCGCGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATG  
GAGCCATGCATCTCCATGACTACAAGTCAGATGTACCAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG  
ATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG  
ACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACC  
TGGGGGAGCCAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCCCT  
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG  
TGTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT  
ACACCGTGTGAGGATCTTGGTGGAGAATCGTGGGCGAGTCAACTATGGGGAGAATATTGATGACCAGCGCAAAG  
GCTTAATTGGAAATCTCTATCTGAATGATTACCCCTGAAAACCTTCAAGATCTATAGCCTGGATATGAAGAAGA  
GCTTCTTTTCAAGGTTTCGGCTTGGACAAATGGNGTTCCCTCCAGAAAACCCACATTACCTGCTTTCTTCTTGG  
GTAGCTTGTCCATCAGCTCCACGCCTTGTGACACCTTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTGTATTCA  
TCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCCAAGACGCTTTACCTCCCAGGTCCCTGGTTGA  
GCAGCGGAATCAACCAGGTCATCGTTTTGGAGGAGACGATGGCGGGCCCTGCATTACAGTTTACGGAAACCCCCC  
ACCTGGGCAGGAACCACTACATTAAGTGAAGCGGTGGCACCCCTCCTGCTGGTGCCAGTGGGAGACTGCCGCCTC  
CTCTTGACCTGAAGCCTGGTGGCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGG  
ACTGGGGGCTACAGTCTGCCCCGTGTCTCAGCTCAAAACCCCTAAGCCTGCAGGGAAAGGTGGGATGGCTCTGGGC  
TGGCTTTGTTGATGATGGCTTTCCTACAGCCCTGCTCTTGTGCCGAGGCTGTTCGGGCTGTCTTAGGGTGGGAGC  
AGCTAATCAGATCGCCAGCCCTTGGCCCTCAGAAAAAGTGCTGAAACGTGCCCTTGACCCGACGTCAACAGCCC  
TGCGAGCATCTGCTGGACTCAGGCGTGCTCTTGTCTGGTTCCTGGGAGGCTTGGCCACATCCCTCATGGCCCCAT  
TTTATCCCCGAAATCCTGGGTGTGTACCAGTGTAGAGGGTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT  
CTTCCCTTCAACCTTCTGAGCCTTCTTTGGGATTCTGGAAGGAACTCGGCGTGAGAAACATGTGACTTCCCCCTT  
TCCCTTCCCACTCGCTGCTTCCCACAGGGTGACAGGCTGGGCTGGAGAAAAGAAATCCTCACCTGCGTCTTCC  
CAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCCCATGTCTGCA  
CATCCAGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCCATGTCTGCACATCC  
AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCCATGTCTGCACATCCAGGGA  
GGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCCATGTCTGCACATCCAGGGAGGAGG  
ACAGAAGGCCAGCTCAGTGGCCCCCGCTCCCCACCCCCACGCCGAACAGCAGGGGACAGCAGCCCTCCTTC  
GAAGTGTGTCCAAGTCCGATTTGAGCCTTGTCTGGGGCCAGCCCAACACCTGGCTTGGGCTCACTGTCTCTGA  
GTTGCAGTAAAGCTATAACCTTGAATCACAA

FIGURE 63

## **FIGURE 64**

MTTWSLRRRPPARTLGLLLLVVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW  
IFGGSIHYFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDFSGNLDLEAFVLMA  
AEIGLWVILRPGPYICSEMDLGGLP SWLLQDPGMRLRTTYKGFTEAVDLYFDHLMSRVVPLQ  
YKRGGP IIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLLLTSDNKDGLSKGIVQGVLAT  
INLQSTHELQLLTTF LFNVQGTQPKMVMEYWTGWFD SWGGPHNILDSSSEVLKTVSAIVDAGS  
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDY TAKYMKLRDFFGSGISGIP  
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYILYE  
TSITSSGILSGHVHDRGQVFVNTV SIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN  
IDDQRKGLIGNLYLNDSP LKNFRIYSLDMKKSFFQRFGLDKWXS L PETPTLP AFFLGSLSIS  
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLP GPWLSSGINQVIVFEETMAGPA  
LQFTETPHLGRNQYIK

### **Signal sequence:**

amino acids 1-27

### **Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

### **N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586



## FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC  
CTGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
GGAGCAAAGCCGGGCTCGGCCCCGAGGCCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC  
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC  
AAGAAGCTGTCTTGCCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCA  
GGCAGACACTCGGTCGTTCTAGTGGATAGGGGTCATGACCGGTTTCTCCTAGACGGGGCCC  
CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCGGAC  
CGGCTTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTTATGTGCCCTTGAACTA  
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCCTTCTGA  
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG  
TGGGAGATGGGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC  
AGATCCAGACTTCCTTGCCGAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATC  
CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTGAGGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGGCTCTTCCGTGCACTGCTAGG  
AGAAAAGATCTTGCTCTTCACCACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
GACTCTATAACACTGTAGATTTTGGCCCAGCTGACAAACATGACCAAAATCTTTACCTGCTT  
CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA  
CTGGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC  
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG  
AATGGTGGCGATAAGAAGGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTTGCTCTTCGAGATGTCATCAGCAAGT  
TCCAGGAAGTTCCTTTGGGACCTTTACCTCCCCCGAGCCCCAAGATGATGCTTGGACCTGTG  
ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCCCAT  
TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC  
GAACCTATATGACCCATAACATTTTTGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTC  
CATGACCGTGCCCTATGTGATGGTGGATGGGGTGTTCCAGGGTGTGTGGAGCGAAATATGAG  
AGACAAACTATTTTTGACGGGGAAACTGGGGTCCAAACTGGATATCTTGGTGGAGAACATGG  
GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG  
GGGCAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG  
GTGGTTTTCCCTCCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT  
ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG  
ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACTTGGGCCGGTACTGGACAAAGCAGGGGCC  
ACAACAGACCTCTACGTGCCAAGATTCCTGCTGTTTCTAGGGGAGCCCTCAACAAAATTA  
CATTGCTGGAAC TAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTTGGATAAGCCTATC  
CTCAATAGCACTAGTACTTTGCACAGGACACATATCAATTCCCTTTCAGCTGATACACTGAG  
TGCTCTGAACCAATGGAGTTAAGTGGGCACTGGAAGGTAGGCCGGGCATGGTGGCTCATGC  
CTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAGGACTTCAAGA  
CCAGCCTGGCCAACATGGTGAAACCCGTCTCCACTAAAAATACAAAATTAGCCGGGCGTG  
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC  
AGGAGGCAGAGGTTGCAGTGAGTGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA  
GACACTCCATCTCAAAAAAAAAAAAA

00446-0130

## **FIGURE 66**

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLMKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDGFPADNMTKIF  
TLRLKYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMFMFHGGTNF  
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL  
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

### **Signal sequence:**

amino acids 1-27

### **N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

### **Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

### **Tyrosine kinase phosphorylation site.**

amino acids 191-198

### **N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## FIGURE 67

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC  
ACCCACAATATGGCCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT  
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTTCAGGATACCTTTGAAGGAATATT  
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT  
GCGTTCCTTCTTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTTGGTGTGTT  
CTTGTCAGAAGTTAGTGAAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG  
AAAAACTCAGGCAGCACATTTACGCAACGCCCAGGACAAGCAGGAGTTGCATCTGTTCATG  
CTGTCGGGGGTGCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCCAGAAGCTAAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA  
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAA  
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTTCTCCACGTGAAGAGCAATTTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTCATAATGACGGCAC  
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA  
ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACTGGAT  
TTAAAGTCCAATAACATTTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAACGACT  
GACTTGTTTTAAAATTATGGCATAACAAAATTGTTACTATTCTCCCTCTATTACCCATGTCA  
AAAACCTTGAGTCACTTTATTTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT  
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAAGTGGACATTCTGC  
CAAAACAATTGTTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC  
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCCAGCTCACTCAGCTGGAGCTGAAGGGGAACTG  
CTTGGACCGCCTGCCAGCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAGCGGGCTTGTTG  
TGGAAGATCACCTTTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA  
AATATTCCTTTGCAAATGGGATTTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC  
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG  
ATACATCTTTTAAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTTGTAGGGTTTTAAGTCATTCATTTCCAAATCATTTTTTTTTTTCTTTTGGGG  
AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTTCTTTTTTAAATTGTTTGTAACCTGGAT  
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAAAAAAAAAAAAAA

## **FIGURE 68**

MAYMLKKLLISYISIIICVYGFI~~C~~LYTLFWLFRIP~~L~~KEYSF~~E~~KVREESSFSDIPDVKNDF~~A~~FL  
LHMVDQYDQLYSKRFGVFLSEVSENK~~L~~REISLNHEWTFEKL~~R~~QHISRNAQDKQELHLF~~M~~LSG  
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPAWVYLLKNLRELYLIGNLSEN~~N~~KMIGLES~~L~~RELRLHLKILHVKS~~N~~LTKVPSN  
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAE~~L~~ELQNC~~E~~LERIPHAIFSLSNLQELDLKS  
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLES~~L~~YFSNNKLES~~L~~PVAVFSLQ  
KLRC~~L~~DVSYNNISMIP~~I~~EIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP  
EKVGQLSQLTQLELKGNC~~L~~DR~~L~~PAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP  
FANGI

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

### **Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

### **Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

### **N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## FIGURE 69

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCCATTCTTTTCATTGACAACTGACTTTTTTTTATTTCT  
TTTTTTCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATAAGGAT  
CTGTGTTTGGGGTTTCTTCTTCTCCCTGACATTGGCATTGCCTAGTGGTTGTGTGGGGAGGGAGACCACGTGG  
GCTCAGTGCCTTGCCTGCACTTATCTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTC  
ATCGCTGGTGGTATCCTGGCGGCCTTGCTCCTGCTGATAGTTGTCTGTCTTTACTTCAAATAACACAAC  
GCGCTAAAAGCTGCAAGGAACCTGAAGCTGTGGCTGTAAAAATCACAACCCAGACAAGGTGTGGTGGGCCAAG  
AACAGCCAGGCCAAAACCATTGCCACGGAGTCTTGTCTGCCCCTGCAGTGTGTGAAGGATATAGAATGTGTGCC  
AGTTTTGATTCCCTGCCACCTTGCTGTTGCGACATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAA  
GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAG  
CTCCCCATCAGTTTCATGGAAAATAACTCAGTGCCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAGAGCTTC  
CACTGGGGGCAACCCCTCCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGGAATGCTGATAAACAGTCA  
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCTGGAAGTACGTTTCCCTGGAGGTGTCCAGAAA  
GCTGATGTAACACAGAGCCTATAAAAGCTGTGGTCTTAAGGCTGCCAGCGCCTTGCCAAAATGGAGCTTGTGA  
AGAAGGCTCATGCCATTGACCTCTTAATTCTCTCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAAT  
GCAAGCTGCACAGTCACTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC  
AGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAGCATCAGAATTATCTTTTCTATGTCCAGCTT  
GATCCAGATGGAAGCTGTGAAAGTGAAAACATTAAAGTCTTTGACGGAACTCCAGCAATGGGCCTCTGCTAGGG  
CAAGTCTGCAGTAAAAACGACTATGTTCTGTATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT  
GACTCAGCAAGAAATTCAAAGAAGTGTCTTTGTCTTCTACTACTTCTTCTCTCTTAACATCTCTATTCCAACTGT  
GGCGGTTACCTGGATACCTTGGAAAGGATCCTTACCAGCCCCAATTACCCAAAGCCGCATCCTGAGCTGGCTTAT  
TGTGTGTGGCACATACAAGTGAGAAAGATTACAAGATAAACTAACTTCAAAGAGATTTTCTAGAAATAGAC  
AAACAGTGCAAAATTTGATTTTCTTGCCATCTATGATGGCCCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGT  
GGCCGTGTGACTCCACCTTCGAATCGTCATCAAACCTCTGACTGTCTGTGTGTCTACAGATTATGCCAATTCT  
TACCGGGGATTTTCTGCTTCTTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTTCT  
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAATAACTTGCAACTAAAA  
GACCCAACTTGCAGACCAAAATTATCAAATGTTGTGGAATTTTCTGTCCCTCTTAATGGATGTGGTACAATCAGA  
AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACC  
CGTCAGAAACAACCTCCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA  
GAAGATGATGTAATACAAAGTCAAAATGCACTGGGCAAAATATAACACCAGCATGGCTCTTTTGAATCCAATTCA  
TTTGAAGAGACTATACTTGAATCACCATATTATGTGGATTTGAACCAAACCTTTTTTGTTCAGTTAGTCTGCAC  
ACCTCAGATCCAAATTTGGTGGTGTCTTGTGATACCTGTAGAGCCTCTCCACCTCTGACTTTGCATCTCCAACC  
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTTGTAAAGGTGTATCCCTTATTTGGACACTATGGGAGA  
TTCCAGTTTAAATGCCTTTAAATTTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAGTTTTGATATGTGAT  
AGCAGTGACCACCAGTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAAACGAGACATTTCTTCATATAAATGG  
AAAACAGATTCATCATAGGACCCATTTCGTCTGAAAAGGGATCGAAGTGCAAGTGGCAATTGAGGATTTTTCAGCAT  
GAAACACATGCGGAAGAACTCCAAACCAGCCTTTCAACAGTGTGCATCTGTTTTCTTTCATGGTTCTAGCTCTG  
AATGTGGTGACTGTAGCGACAATCACAGTGAGGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTG  
CAGAAGTATTAACAGGTCCAACCTAAGTGAGACATGTTTCTCAGGATGCCAAAGGAAATGCTACCTCGT  
GGCTACACATATTATGAATAAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGTAAAAAA

## **FIGURE 70**

MELVRRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIFSYVQLDPDGSCSENIKVFDGTSSNGPLLQGVCCKNDYVPVFESSSSSTLT  
FQIVTDSARIQRTVFVFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIIISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST  
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTIKLESPYYVDLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL  
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFGHETHA  
EETPNQPFNSVHLFSFMVLALNVTVATITVRHFVNQRADYKYQKLQNY

### **Signal sequence:**

amino acids 1-24

### **Transmembrane domain:**

amino acids 571-586

### **N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

### **Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

### **Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

### **N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

Figure 1 consists of 12 histograms arranged in a single column. Each histogram represents the distribution of the number of non-zero elements in the vector  $x$  for a specific value of  $n$ . The x-axis for all histograms is labeled 'x' and ranges from 0 to 120. The y-axis is labeled 'count' and ranges from 0 to 100. The histograms are for  $n = 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120$ . As  $n$  increases, the distribution of non-zero elements shifts to the right, indicating that more elements in the vector  $x$  are non-zero for larger  $n$ . The peak count for each distribution decreases as  $n$  increases.

GACCGAAGAACACAGCGCTCCCGAGGGCCGCGGGAGGCTGCAGAGAGGACAGCCGGCCTGCGCCG  
 GGACATGCGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGC  
 TGCTGCCGCCGCCGCGCTGCCCTGCCACAGCGCCACGCGCTTCGACCCACCTGGGAGTCC  
 CTGGACGCCCCGCCAGCTGCCCGCGTGGTTTTGACCAGGCCAAGTTCGGCATCTTTCATCCACTG  
 GGGAGTGGTTTTCCGTGCCAGCTTTCGGTAGCGAGTGGTCTGGTGGTATTGGCAAAGGAAA  
 AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAATATGAAGAT  
 TTTGGACCACTATTTACAGCAAAATTTTTTAATGCCAACAGTGGGCAGATATTTTTTCAGGC  
 CTCTGGTGCCAAATACATTGTCCTTAACCTTCAAACATCATGAAGGCTTTACCTTGTGGGGGT  
 CAGAATATTTCGTGGAACCTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA  
 CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTTGGACTGTACTATTCCTTTTTTGA  
 ATGGTTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG  
 TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG  
 TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT  
 ATATAATGAAAGCCCAGTTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA  
 TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA  
 CATAAATGGGAAAACCTGCATGACAATAGACAAACTGTCTCTGGGGCTATAGGAGGGAAGCTGG  
 AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTCATGTG  
 GAGGAAATCTTTTGATGAATATTGGGCCCACACTAGATGGCACCATTTCGTAGTTTTTTGAG  
 GAGCGACTGAGGCAAGTGGGGTCTTGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA  
 TACCTGGCGATCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG  
 AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCACATCAGGACAGCTGTTCTTGGCCAT  
 CCCAAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG  
 GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTTCATCAGATGC  
 CGTGTAATATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG  
 ATGCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA  
 AAGCAATGTAAACTGGATAAGAAAATTATTTGGCAGTTCAGCCCTTTCCCTTTTTTCCACTA  
 AATTTTTCTTAAATTACCCATGTAACCATTTTTAACTCTCCAGTGCACCTTTGCCATTAAAGTC  
 TCTTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTTCACATTATAGTAG  
 CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCCATG  
 ATTATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAAT  
 TTTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA  
 CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG  
 AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAAACATAGAGAAG  
 GTACAGTAAAAATACTGTAAATAAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG  
 CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA  
 TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAAA  
 GTTTTTCTTTCTTCAATTATAAATTAACATAAGTGTACTGTAACTTTACAAACGTTTTTAATT  
 TTTAAACCTTTTTTGGCTCTTTTGTAATAACACTTAGCTTAAACATAAACTCATTGTGCAA  
 ATGTAA

## **FIGURE 72**

MRPQELPRLAFPLLLLLLLLLLPPPPCPAHSATRFDPWESLDARQLPAWFDQAKFGIFIHWG  
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLEFW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGKNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT  
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKKGWALALTNVI

### **Signal sequence:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

### **Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

### **Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

### **N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

### **Leucine zipper pattern.**

amino acids 410-432

### **Alpha-L-fucosidase putative active site.**

amino acids 283-295

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## FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT  
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC  
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTTG  
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGAGCT  
TTCCATCCAGGTGTCTATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACCAGC  
AGCTGAATTTACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG  
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGGAGA  
TGGATTTCGTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG  
TCCTGATTTTGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGAT  
ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCA  
AACTGCAACACAAACAACAGAATTTATTGTCTAGTGACAGTACCTACTCGGTGGCATCCCCTT  
ACTCTACAATACTGCCCCCTACTACTCTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG  
AGAAAAAATTGATTTGTGTACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAAAC  
TGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCC  
CCACGGCTCTGCTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGC  
TATGTCAAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT  
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGA  
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAA  
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCC  
TTACCCTGCCCCAGCTGGGGAAATCAAAAGGGCCAAAGAACCAGAAAGTCCACCCTT  
GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC  
CCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC  
TTTCTAGCCTGGCTATGTCTAATAATATCCCACTGGGAGAAAGGAGTTTTTGCAAAGTGCAA  
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGG  
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGAC  
CCTTCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTA  
AGAGCAAAAGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAG  
ACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT  
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGA  
ATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCT  
AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCA  
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT  
TGAATATTATTCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTCA  
GTTTTGATATTTCTAGCTTATCTACTTCCAACTAATTTTTTATTTTTGCTGAGACTAATCTT  
ATTCATTTTCTCTAATATGGCAACCATATAACCTTAATTTATTATTAAACATACCTAAGAAG  
TACATTGTTACCTCTATATACCAAAGCACATTTTAAAAGTGCCATTAACAAATGTATCACTA  
GCCCTCCTTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAA  
AGCATTTAGAAAACCTT

TCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG

## **FIGURE 74**

MARCFSLVLLLLTSIWTTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLWKPVSQRQF  
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAFPFTNKNQOKEMIETKVVKEEKANDSNPNEESKKTDKNPESKSP  
SKTTVRCLAEV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

### **Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

### **Tyrosine kinase phosphorylation site.**

amino acids 79-88

### **N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

[illegible]

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGATTTCGGTGCCGCACTTTTACGATGAACTCTGCCCCAACCTTACTACCTTCTGTGCGGCCCTGCTCTCTGCTGCCTTCCTACTCGTGAGGAACTGCGCGCGCTCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTGACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGATCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTTAGTAAAGTGGCCAACACAATTCTTTTCTTCCGCTTGGATATTCGCATGGGCCTACTTTACATCACACTCTGCATAGTGTTCCTGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAAACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAATTGGTCTAATGACTGCCAATCATTGCCCCCTATCTATGCTGACCTCTCCCTTAAATACAACGTACAGGGCTAAATTTTGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTACAAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAAGGAGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTGAGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCAAAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTCAGATGGGGAAAAACAAGAAGGATAAATAAGATCCTCACTTTGGCAGTGCTTCCTCTCCTGTCAATTCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGGCTGNGACTGGNTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAGGCACCTACAGGAAGGCCTGCCATGCTGTGGCCAACGTGTTTCACTGGAGCAAGAAAGAGATCTCATAGGACGGAGGGGGAAATGGTTTTCCCTCCAAGCTTGGGTCAGTGTGTTAACTGCTTATCAGCTATTACAGACATCTCCATGGTTTTCTCCATGAAACTCTGTGGTTTCATCATTCCTTCTTAGTTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAACGCTAAGAATTTTCCCCCAAGGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTCTTCATTAAAAGTATAAGCCTAACTTTGTCGCTAGTCCTAAGGAGAAACCTTTAACCACAAAGTTTTTTATCATTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAATAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCCTGGACTTTCACTAACCCTCTGACATACTCCCCACACCCAGTTGATGGCTTTCGGTAATAAAAAGATTGGGATTTCCTTTTG

## **FIGURE 76**

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVVRKLPPLCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC  
TGLNFGKVDVGRYTDVSTRYKVSTSPSTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

### **Signal sequence:**

amino acids 1-48

### **Transmembrane domain:**

amino acids 111-125

### **N-glycosylation site.**

amino acids 165-169, 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

### **N-myristoylation site.**

amino acids 188-194, 225-231

### **Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

[illegible][illegible]

## **FIGURE 78**

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR  
HRR LHRYDVFCFATALKGRVYYLEHPEKLTLTAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVHHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

### **Signal sequence:**

amino acids 1-17

### **Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

### **Tyrosine kinase phosphorylation site.**

amino acids 137-145

### **N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

[illegible]

## **FIGURE 80**

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ  
FRDFRDLNKGHLDGSEVGHVWLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 140-144

### **Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

### **N-myristoylation site.**

amino acids 263-269, 311-317

### **Endoplasmic reticulum targeting sequence.**

amino acids 325-330



## FIGURE 81

GGGGCCTTGCCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG  
GCGGCGGGCGCGGGTGCGAGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTGCTCCAG  
CCTGTCTGTGTCGTGTTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTTGCACACCGATCCTG  
GGCTTCGCTCGATTTGCCGCCGAGGCGCCTCCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG  
CGGGTCGTCTGTGTCCTCTCTCCTCTGCGCCGCGCCCCGGGGATCCGAAGGGTGCGGGGCTCT  
GAGGAGGTGACGCGCGGGGCCTCCCGCACCCCTGGCCTTGCCCGCATTTCTCCCTCTCTCCAG  
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCCGGCTCTCGGCCTCGGTGTG  
TGTCTGCTGCTGCTGCGCGGGGCCCCGCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG  
TTTTACCAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCCAGGGGGCTGCC  
CTCTTGAGGAATTTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG  
GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACC  
TGGTCGAGAAAACCTATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT  
GGTCTGCTTCTTTTACAGTAACTAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACCTGG  
CAATAAAGATTGTAAAGCAGACATTTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC  
GCCGATTTAATTTACAGAAGAATTTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA  
GAAGGACCACATGTGGGCCTTGTTCAGCCAGTGAACATCCCAAATAGAATTTTACTTGAA  
AACTTTTACATCAGCCAAAGATGTTTTGTTTGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA  
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTTCACGGTAGATGCTGGA  
GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACAT  
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA  
AGCCTATCCCTGAAGAACTGGGGATGGTTTCAGGATGTCACATTTGTTGACAAGGCTGTCTGT  
CGGAATAATGGCTTCTTCTCTTACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAAA  
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT  
CAGTGAACATTGCCTTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCTC  
ATGCTTGAATTTGTTTTCCAACATAGCCAAGACTTTTGAAATCTCGGACATTGGTGCCAAGAT  
AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTCAGTTTCACTGACTATAGCACCA  
AAGAGAATGTCCTAGCTGTCTATCAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT  
GATGCCATTTTCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAAAGAA  
CTTCCTAGTAATTTGTACAGATGGGCAGTCCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG  
CACATGATGCAGGAATCACTATCTTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG  
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTTCTTCACAAGAGAGTTCACAGGATT  
AGAACCAATTGTTTTCTGATGTCATCAGAGGCATTTGTAGAGATTTCTTAGAATCCCAGCAAT  
AATGGTAACATTTTGACAACCTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAAATTGTATT  
CTCATAATACTGAAATGCTTTAGCATACTAGAATCAGATACAAAACCTATTAAGTATGTCAAC  
AGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT  
ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAACTCAGGAAAGAGGA  
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA  
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAAAA

## **FIGURE 82**

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEFVS  
VYGNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTTFVDKAVCRNNGFFSYHMPNWF GTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI  
DGSSSVGDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI  
FSVGVAWAPLDDLKDMASKPKESHAF FTREFTGLEPIVSDVIRGICRDFLESQQ

### **Signal sequence:**

amino acids 1-24

### **N-glycosylation site.**

amino acids 100-104, 221-225

### **Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

### **N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

### **Amidation site.**

amino acids 145-149

## FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCAGCCC  
GGCGGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCCGAGCGCAACTCGGTCCAGTCG  
GGGCGGCGGCTGCGGGCGCAGAGCGGAGATGCAGCGGCTTGGGGCCACCCTGCTGTGCCTGC  
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTC  
AAGCCCGGCCCGGCTCTCAGCTACCCGCGAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGA  
GGTTGAGGAACTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG  
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTAT  
CACAATGAGACCAACACAGACACGAAGGTTGGAAATAATACCATCCATGTGCACCCGAGAAAT  
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGGCCAGC  
ATGTACTGCCAGTTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCT  
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAAA  
TGGCCACCAGGGGCAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGGCTG  
TGCTGTGCCTTCCAGAGAGGCCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGA  
GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATG  
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGTGCC  
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG  
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCCGCCGCT  
GCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA  
ATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCTTACA  
TCTTCTTCCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTACG  
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAAC  
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAG  
ACAGCCGTTTGTCTACATGGCTTTGATAATTGTTTGAAGGGAGGAGATGGAAACAATGTGG  
AGTCTCCCTCTGATTGGTTTTTGGGGAAAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAA  
CCTGGCAAAAATGCAACAAATGAATTTTCCACGCACTTCTTTCCATGGGCATAGGTAAGCTG  
TGCTTTCAGCTGTTGCAGATGAAATGTTCTGTTACCCTGCATTACATGTGTTTATTCATCC  
AGCAGTGTTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATTC  
CCTCTCTCAGCACAGCCTGGGGAGGGGGTCATTGTTCTCTCGTCCATCAGGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCAT  
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA  
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTCTTGAGGCATGCACATCTGGAATTAAG  
GTCAAATAATTCTCACATCCCTCTAAAAGTAACTACTGTTAGGAACAGCAGTGTTCTCAC  
AGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGT  
TGCATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA  
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAATCACTTAGCAGCAAC  
TGAAGACAATTATCAACCACGTGGAGAAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT  
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTTTCAGGTGTCA  
TGGACTGTTGCCACCATGTATTATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGATTGTA  
TAAGCATGCTTTCTTTGAGTTTTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGC  
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 84**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ  
HKLRSAVEEMEAEAAAKASSEVNLANLPSPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMMLCTRDSECCG  
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV  
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEEI

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

### **N-myristoylation site.**

amino acids 202-208, 217-223

### **Amidation site.**

amino acids 140-144

## FIGURE 85

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGGCTCAGAAGGACTCTG  
AAGATAACAATAATTTTCAGCCCATCCACTCTCTTCCCTCCCAAACACACATGTGCATGTACACACACACATACA  
CACACATACACCTTCTCTCTCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACAC  
TAAAGCCTTAAGGACAGGCTGGCCATTACCTCTGCAGCTCCTTTGGCTTGTGAGTCAAAAAACATGGGAGGGG  
CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTCAGGAG  
TTCGAGACCAGCCTGGCCAAACATGGAGAAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGAGTGGTGGC  
AGGTGCCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGT  
CAGCTGAGTGCACCGCTGCCTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA  
GGGCTAGATACTGCTTCTCTGCAACCTCCTTAACCTGTCATCCTCTTCTCCAGGGCTGCCCCCTGATGGGGCCTG  
GCAATGACTGAGCAGGCCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGACGCCCG  
GTGTAGAAATGACTGCCCTGGGAGGGTGGTTCTTGGGCCCTGGCAGGGTGTGCTGACCCTTACCCTGCAAAACACA  
AAGAGCAGGACTCCAGACTCTCCTTGTGAATGGTCCCCTGCCCTGCCAGCTCCACCATGAGGCTTCTCGTGGCCCC  
ACTCTTGCTAGCTTTGGGTGGCTGGTGCCACTGCCCTGCTGCCCTGGTACCTGGCATGTTCCCTGCCCCCTCA  
GTGTGCCCTGCCAGATCCGGCCCTGGTATACGCCCCGCTCGTCTACCGCGAGGCTACCACTGTGGACTGCAATGA  
CCTATTCTGACGGCAGTCCCCCGGCACTCCCCGAGGCACACAGACCCTGCTCCTGCAGAGCAACAGCATTGT  
CCGTGTGGACCAGAGTGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCAGAACAGCTTTTCGGA  
TGCCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTGAGCCTGCACCTAGAGGAGAACCAGCTGACCCGGCT  
GGAGGACCACAGCTTTGACAGGGCTGGCCAGCCTACAGGAACCTATCTCAACCACAACCAGCTTACCGCATCGC  
CCCCAGGGCCTTTTCTGGCCTCAGCAACTTGTCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAG  
CCGCTGGTTTGAATGCTGCCCAACTTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATCTCGGACAT  
GAACCTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGTAGCAGGCATGAACCTGCGGGAGATCTCCGACTATGC  
CCTGGAGGGGTGCAAAGCCTGGAGAGCCTCTCCTTCTATGACAACCAGCTGGCCCCGGGTGCCCAGGCGGGCACT  
GGAACAGGTGCCCGGGCTCAAGTTCTTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGC  
CAACATGCTGCACCTTAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGCCCTGGT  
GAACCTCCCCGAGCTGACCAAGCTGGACATCAACAATAACCCACGGCTGTCTTTCATCCACCCCCCGCCTTCCA  
CCACCTGCCCCAGATGGAGACCCTCATGCTCAACAACAACGCTCTCAGTGCCTTGCACCAGCAGACGGTGGAGTC  
CCTGCCAACCTGCAGGAGGTAGGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTATCCGCTGGGCCAATGC  
CACGGGCACCCGTGTCCGCTTCTCGAGCCGCAATCCACCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC  
GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGGCCCTCATCTCCCCACGAAGCTTCCCCCAAG  
CCTCCAGGTAGCCAGTGGAGAGCATGGTGTGCTGCTTGGCCGGCACTGGCCGAACCCGAACCCGAGATCTACTG  
GGTCACTCCAGCTGGGCTTCGACTGACACCTGCCCCATGCAGGCAGGAGGTACCGGGTGTACCCCGAGGGGACCT  
GGAGCTGCGGAGGGTGACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCAGAACCTGGTGGGGGCTGACAC  
TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACAGGGGCTGGAGCTCCG  
GGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTCACCCCACCCAACACAGTGTCCACCAACCTCAC  
CTGGTCCAGTGCCCTCCTCCTCCGGGGCCAGGGGGCCACAGCTCTGGCCCGCCTGCCTCGGGGAACCCACAGCTA  
CAACATTACCCGCCTCCTTCAGGCCACGGAGTACTGGGCCCTGCCTGCAAGTGGCCTTTGCTGATGCCCCACACCCA  
GTTGGCTTGTGTATGGGCCAGGACCAAAGAGGCCACTTCTTGCCACAGAGCCTTAGGGGATCGTCTGGGCTCAT  
TGCCATCCTGGCTCTCGTGTCTTCTCCTGGCAGCTGGGCTAGCGGCCACCTTGGCACAGGCCAACCCAGGAA  
GGGTGTGGGTGGGAGGCGGCCCTCCTCCTCCAGCCTGGGCTTTCTGGGGCTGGAGTGCCCCCTTCTGTCCGGGTGT  
GTCTGCTCCCCCTCGTCTGCCCTGGAATCCAGGGAGGAAGCTGCCCAGATCCTCAGAAGGGGAGACACTGTTGCC  
ACCATTTGTCTCAAAATTTCTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTTACCAAA  
AGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGCCTGGCAGCTGGGC  
CAAGACAGATGGGGCTTTGTGGCCCTGGGGGTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTCA  
CCTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCTCCCCATCTT  
CTCTCTGCCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCTACCTGTGTCCCCGGGCTGCACCCCTTCTCTTCT  
TCTTTCTCTGTACAGTCTCAGTTGCTTGTCTTGTGCTCCTGGGCAAGGGCTGAAGGAGGGCACTCCATCTCAC  
CTCGGGGGGCTGCCCTCAATGTGGGAGTGACCCACAGCAGATCTGAAGGACATTTGGGAGAGGGATGCCCAGGAA  
CGCTCATCTCAGCAGCCTGGGCTCGGCATTCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTTGTGGAGAA  
ATGTGTACCTCCCCCAACCCGATTCACTCTTTCTCCTGTTTGTAAAAAATAAAAAATAATAATAACAATAAA  
AAAA

FIGURE 85

## **FIGURE 86**

MRLLVAPLLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA  
VPPALPAGTQTLLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQ  
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNL  
ELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNALSALHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ  
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAEAGLYT  
CVAQNLVGADTKTVSVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW  
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAILALAVLLLAAGLAHLGTGQPRKGVGGRRPLPPAWAFWGSAPSVRVV  
SAPLVLPWNPGRKLP RSSEGETLLPPLSQNS

### **Signal sequence:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 629-648

### **N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

### **Tyrosine kinase phosphorylation site.**

amino acids 532-540

### **N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

### **Amidation site.**

amino acids 470-474, 660-664, 692-696

# FIGURE 87

GCAAGCCAAGGCGCTGTTTGTAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT  
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA  
CATCAAGTTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCCACCC  
CCTGGCCACACTCTTCAAGATCCTGGCGTCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA  
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG  
CGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA  
GCGCTTCGCGCTCTTCTGTGCGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGTGGACGCT  
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCAT  
CCCTGACACTGTGTTTGAACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGC  
CAGCATTGCCAGCTCACGGGCTCAAGGAGCTGTGGCTTACCACACAGCGGCCAAGATTGAAGCGCCTGCGCT  
GGCCTTCCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCGCTGTGGATCTA  
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAACCGCTACATCGTCATCGA  
CGGGCTGCGGGAGCTCAAACGCCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCAC  
AGATGTGGGCGTGCACCTGCAGAAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCTCAACAGCCTCAA  
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT  
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCT  
GCACCGCCTCACCTGCCTTAAGCTGTGGTACAACCACATCGCCTACATCCCCATCCAGATCGGCAACCTCACAA  
CCTGGAGCGCCTTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCG  
CTACCTGGACCTCAGCCACAACAACCTGACCTTCTTCCCTGCGCAGATCGGCCTCCTGCAGAACCTCCAGAACCT  
AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCT  
GGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGG  
CAACCGGCTGGAGTGCCTGCCTGTGGAGCTGGGCGAGTGCCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGA  
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCCTGAGCGAG  
GCCGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCCGAGGGGCGAGGCCCTAGCTTCTCCAG  
AACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCGAGGAGCCTGGGGCCGCTTGTGAGTCAGGCCAGAGCGAGA  
GGACAGTATCTGTGGGCTGGCCCCCTTTCTCCCTCTGAGACTCAGTCCCCCAGGGCAAGTGCTTGTGGAGGAG  
AGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTCTGCCCCAGGGGCTGAG  
CTGCCACCAGAGGTCTGGGACCCCTCACTTTAGTTCTTGGTATTTATTTTTCTCCATCTCCACCTCCTTCATCC  
AGATAACTTATACATTCCCAAGAAAGTTTACGCCAGATGGAAGGTGTTTCAAGGAAAGGTGGGCTGCCTTTTCCCC  
TTGTCTTTATTTAGCGATGCCGCCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCGAACCAG  
CCATGGGACGGTCAACCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCCCTCCAGCTGGA  
AAGGCCAGGCCCTGGAGCTTGCCCTCTTCAAGTTTTGTGGCAGTTTTAGTTTTTTTTTTTTTTTTTAAATCAAA  
AAACAATTTTTTTTTAAAAAAGCTTTGAAAATGGATGGTTTGGGTATTAAGGAAAAAAGAAAAAAGCTTAAAAA  
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAAAGCAGCCAGACGT  
TGAAGTGTGTTTTCTTTCCCTGGGCGCAGGGTGCAGGGTGTCTCCGATCTGGTGTGACCTTGGTCCAGGAGTT  
CTATTTGTTCTTGGGGAGGGAGGTTTTTTTGTTTTGTTTTTTGGGTTTTTTTGGTGTCTTGTTTTTCTTCTCCTCC  
ATGTGCTTTGGCAGGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG  
ACTCGGGTTGGCTAATCCCCGGATGAACGGTGTCCATTCGCACCTCCCCCTCCTCGTGCTGCCCTGCCTCTCCA  
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTCGCCCAGACTTTGTTTCCCCACCTCCTGCGGCATGGGTGTGT  
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTGCGCCACCTGGTCTTTCATGAAGAGCAGACACTTA  
GAGGCTGGTCCGGAATGGGGAGGTGCCCCCTGGGAGGGCAGGCGTTGGTTCCAAAGCCGGTTCCCGTCCCTGGCGC  
CTGGAGTGCACACAGCCAGTCCGCACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTT  
AGAAGGGTCCCCGCCCTTAGATCAATCAGTGGACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATGT  
CCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCGTCTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG  
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAAA  
ATCTATAACAGAAAAA

Figure 87

## **FIGURE 88**

MRQTIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMRLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDTVFDLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRLALHIKFTDIKEIPLWI  
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFQ  
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKRLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPPELFQCRKLRLALHLGNNVLQSLPSRVGELTNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

### **Transmembrane domain:**

amino acids 51-75 (type II)

### **N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

### **Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

### **N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447



## FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCAATGGAGCTGGCACTGCGGCGCTCTCCCGT  
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT  
GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAGGAAATTGGGC  
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT  
GTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG  
AATTCAGACAGTTCATTCTACATTTTCTCAGAGTCTTATGGAGGAAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT  
TGCCTTGGGTGATTCTGATCTCCCCTGTTGATTCGGTGCTCTCCTGGGGACCTTACCTGT  
ACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA  
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGGTGAAGTTCTATAACATCTTAACTAAAAGCACTCCCA  
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTGACGCG  
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA  
GCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTG  
GGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAATTTCAGTCAGCTGAAGTGGAAGGCCCTGT  
ACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTC  
TACTGGATTCTGAAAGCTGGTCATATGGTTTCTTCTGACCAAGGGGACATGGCTCTGAAGAT  
GATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT  
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT  
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT  
GGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT  
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

FIGURE 89

## **FIGURE 90**

MELALRRSPVPRWLLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNGGLYRE  
ATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWVRKLKWPPELPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP  
SDQGDMAKMMRLVTQQE

### **Signal sequence:**

amino acids 1-25

### **N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

### **Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

### **N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## **FIGURE 91**

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCGA  
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA  
GGGGAGCCTGCGCCTGTGGGATTCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG  
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCCTATGACATTG  
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG  
GCCCTCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTCGCCATCATAAACA  
ACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG  
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCTT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG  
GTCGGCCCAATCGGCCCCGGTGTCTACACCAATATCAGCCACCACCTTTGAGTGGATCCAGAAG  
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTTTCCCTCT  
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTTGAGCCTACCTGAGCCCATGCAGCCTGGGGC  
CACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTTGTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 92**

MGARGALLLALLLARAGLRKPESQEAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW  
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNG  
LWYQIGVVSWSGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

### **Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

### **N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

### **Amidation site.**

amino acids 33-37

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

### **Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
Male	55.2 (10.5)
Female	56.8 (11.2)
Marital status	
Married	78.5%
Single	21.5%
Education level	
High school or above	65.2%
Below high school	34.8%
Occupation	
White collar	45.1%
Blue collar	54.9%
Income (USD/month)	
< 1000	12.3%
1000-2000	35.7%
2000-3000	28.9%
> 3000	23.1%
Health insurance	
Yes	89.4%
No	10.6%
Comorbidities	
Hypertension	42.1%
Diabetes	18.5%
Cholesterol	31.2%
Smoking status	
Current smoker	15.3%
Former smoker	22.7%
Non-smoker	62.0%
Alcohol consumption	
Regular	8.9%
Occasional	14.5%
Never	76.6%

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
Male	55.2 (10.5)
Female	56.8 (11.2)
Marital status	
Married	78.5%
Single	21.5%
Education level	
High school or above	65.2%
Below high school	34.8%
Occupation	
White collar	45.1%
Blue collar	54.9%
Income (USD/month)	
< 1000	12.3%
1000-2000	35.7%
2000-3000	28.9%
> 3000	23.1%
Health insurance	
Yes	89.4%
No	10.6%
Comorbidities	
Hypertension	42.1%
Diabetes	18.5%
Cholesterol	31.2%
Smoking status	
Current smoker	15.3%
Former smoker	22.7%
Non-smoker	62.0%
Alcohol consumption	
Regular	8.9%
Occasional	14.5%
Never	76.6%

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYQKYLTLNVADLVRPSPLTLHTVQKLLAAGAQQKCHSVITQDFLTCWL  
SIRQAELLLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGGTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWLML  
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

### **Signal sequence:**

amino acids 1-16

### **N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

### **Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

### **Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

### **N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555



## **FIGURE 96**

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG  
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKNANDIGMDYDYA  
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD  
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW  
IKGNYLDCREG

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 93-97, 207-211

### **Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

### **Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

### **N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

### **Serine proteases, trypsin family, histidine active site.**

amino acids 171-177



## FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT  
CTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCCTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC  
ACTGCTGCCCACTGTTTCAAGGACAACCTGAACAAACCATACTGTTCTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGGAACCCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC  
CCCACCCTGTGTATTCTTGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC  
CCCACCCTCAGACCCTGCAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGGCCCCCTCATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCC  
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA  
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG  
CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA  
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCCGCCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCCGAC  
GGCCTCAGGCCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCCCGCCCCAC  
GACTTCCGGCCCCGCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTTAT  
AGGTATTTGTAACCCTGCCCACATATCTTATTTATTCCTCCAATTTCAATAAATTATTTATT  
CTCCAAAAAAAAA

Variable	Mean	Standard deviation	Minimum	Maximum
Age	34.5	10.5	20	65
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	1.5	10	16
Income	15.5	5.5	10	30
Health status	0.5	0.5	0	1
Smoking status	0.5	0.5	0	1
Alcohol consumption	0.5	0.5	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.5	0.5	0	1
Sleep quality	0.5	0.5	0	1
Work satisfaction	0.5	0.5	0	1
Life satisfaction	0.5	0.5	0	1
Overall health	0.5	0.5	0	1
Physical activity	0.5	0.5	0	1
Mental health	0.5	0.5	0	1
Social support	0.5	0.5	0	1
Work-life balance	0.5	0.5	0	1
Financial stability	0.5	0.5	0	1
Family support	0.5	0.5	0	1
Community involvement	0.5	0.5	0	1
Personal growth	0.5	0.5	0	1
Work environment	0.5	0.5	0	1
Healthcare access	0.5	0.5	0	1
Quality of life	0.5	0.5	0	1
Life expectancy	0.5	0.5	0	1
Overall well-being	0.5	0.5	0	1
Physical fitness	0.5	0.5	0	1
Mental clarity	0.5	0.5	0	1
Social connections	0.5	0.5	0	1
Work engagement	0.5	0.5	0	1
Life satisfaction	0.5	0.5	0	1
Overall health	0.5	0.5	0	1
Physical activity	0.5	0.5	0	1
Mental health	0.5	0.5	0	1
Social support	0.5	0.5	0	1
Work-life balance	0.5	0.5	0	1
Financial stability	0.5	0.5	0	1
Family support	0.5	0.5	0	1
Community involvement	0.5	0.5	0	1
Personal growth	0.5	0.5	0	1
Work environment	0.5	0.5	0	1
Healthcare access	0.5	0.5	0	1
Quality of life	0.5	0.5	0	1
Life expectancy	0.5	0.5	0	1
Overall well-being	0.5	0.5	0	1
Physical fitness	0.5	0.5	0	1
Mental clarity	0.5	0.5	0	1
Social connections	0.5	0.5	0	1
Work engagement	0.5	0.5	0	1
Life satisfaction	0.5	0.5	0	1
Overall health	0.5	0.5	0	1
Physical activity	0.5	0.5	0	1
Mental health	0.5	0.5	0	1
Social support	0.5	0.5	0	1
Work-life balance	0.5	0.5	0	1
Financial stability	0.5	0.5	0	1
Family support	0.5	0.5	0	1
Community involvement	0.5	0.5	0	1
Personal growth	0.5	0.5	0	1
Work environment	0.5	0.5	0	1
Healthcare access	0.5	0.5	0	1
Quality of life	0.5	0.5	0	1
Life expectancy	0.5	0.5	0	1
Overall well-being	0.5	0.5	0	1
Physical fitness	0.5	0.5	0	1
Mental clarity	0.5	0.5	0	1
Social connections	0.5	0.5	0	1
Work engagement	0.5	0.5	0	1
Life satisfaction	0.5	0.5	0	1
Overall health	0.5	0.5	0	1
Physical activity	0.5	0.5	0	1
Mental health	0.5	0.5	0	1
Social support	0.5	0.5	0	1
Work-life balance	0.5	0.5	0	1
Financial stability	0.5	0.5	0	1
Family support	0.5	0.5	0	1
Community involvement	0.5	0.5	0	1
Personal growth	0.5	0.5	0	1
Work environment	0.5	0.5	0	1
Healthcare access	0.5	0.5	0	1
Quality of life	0.5	0.5	0	1
Life expectancy	0.5	0.5	0	1
Overall well-being	0.5	0.5	0	1
Physical fitness	0.5	0.5	0	1
Mental clarity	0.5			

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
```

&gt;&lt;subunit 1 of 1, 317 aa, 1 stop

><MW: 33732, pI: 7.90, NX(S/T): 1

MVVS GAPPALGGGCLGTF TSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP  
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA  
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGWGSIQDG  
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPI TEDMLCAGYLEGERDACLGDSGGPLMC  
QVDGAWLLAGIISWGE GCAERNRPGVYISLSAHRSWVEKIVQGVQLRGAQGGGALRAPSQG  
SGAAARS

**Signal sequence:**

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT  
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCCGCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCAC  
AACAAGGAGCGCGGGCGCCGCGGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT  
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC  
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGGAAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC  
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTTGCCTTACCTGGTAACTGAGGCCCCATCCTTCCGGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT  
TGTTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC  
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC  
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTA  
CCTTCCCCAAATCGACCCATGTTCTATCCCCAAATCAGCAGACAAAGTGACAGACAAAACA  
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG  
GGAACCTCCTACCCCATGCCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG  
AGGTCTTGGCCTCAGTTTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTTCCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACA  
AGCCTAGCGTTGTGTCAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA  
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACTCAAAGGG  
TGAAGAGGTCAGCTGTCTCCTGTCTATCTTCCCCACCCGTGCCCCAGCCCCCTAAACAAGATA  
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC  
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACC  
GGGCCCACACCTCTCCTGCCCCCTCCCTCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCT  
CACTGCCTACCTGGCCTGGGGCTGTCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG  
TGTAAGTGGGGATGGGGATTCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC  
TTTGAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAAACCT  
GTCCAACCTGTGAAA

## **FIGURE 100**

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEE  
LAAFAKAYARQCVWGHNKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVWAKTERIGCGSHFCEKLQGVETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC  
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAEASDSRKMGTTPSSLATGIPAFLVTEV  
SGSLATKALPAVETQAPTSLATKDPSPMATEAPPCVTTTEVPSILAAHSLPSLDEEPVTFPKS  
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV  
SGLNSGPGHVWGPLLGLLLLPPLVLGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

# FIGURE 101

GTAAGTGAAGTCAGGCTTTTTCATTGTTGGGAAGCCCCCTCAACAGAATTCGGTCATTCTCCAAGTTATGGTGGACGT  
ACTTCTGTTGTTCTCCCTCTGCTTGTCTTTTTCACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTTTCAT  
CAAGGCAAGTTCATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACTGAACAACAATGAATTGGAGACCATTCC  
AAATCTGGGACCAGTCTCGGCAAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA  
ACATCTGAAAGAGTTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAACTGCATT  
TCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAA  
TTTGGCCAACACACTCCTTGTGTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACT  
GCCCCAAGTGAACATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGG  
TGCTCTGAAGTCTCTGAAAAATGCAAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGGCTGAGCAA  
CATGGAATTTTTCAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCT  
GCAGGAACCTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAG  
TGAGCTGGACCTAACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATAC  
ACTGCACATTTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCTTCCGGGGGCTTTCCAGTTTAAAGACTTT  
GGATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATGAATGGTGTCTTCTCTGGGCTTGACAAAAGCTGAG  
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCA  
TCTAGACCTGAGTGACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCAAAATGAAGAACTGCAACAATT  
GCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAAATGGCTCCACAGTGGGTGGCGGAAAAACAATT  
TCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAAAAGGAAGAAGCATTTTGTCTGTAGCCCA  
TGGCTTTGTGTGTGATGATTTTCCCAAACCCAGATCACGGTTTCAGCCAGAAACACAGTCGGCAATAAAAGGTT  
CAATTTGAGTTTCATCTGCTCAGCTGCCAGCAGCTGATTCCCCAATGACTTTTGTCTGGAAAAAAGACAATGA  
ACTACTGCATGATGCTGAAATGGAAAAATTAATGCACACCTCCGGGCCCCAAGGTGGCGAGGTGATGGAGTATACCAC  
CATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCTCCAATCACTTTGGTT  
ATCCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCAT  
CCGAGCTGGGGCCATGGCAGCTTGGAGTGTGCTGTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA  
TGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCGAGGATGACGTGTTCTTTATCGT  
GGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTAGCAAAATGC  
AACTCTGACTGTCTTAGAAACACCATCATTTTTCGGGCCACTGTTGGACCCGAACTGTAACCAAGGGAGAAACAGC  
CGTCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAACTGAACTGGACCAAAGATGATAGCCCATTTGGTGGT  
AACCAGAGAGGCACTTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGGAA  
ATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAAC  
CTGCGACTCCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCTGTATCATAGC  
CGTGGTTTTGCTGTGTGGTGGGCACGTCACTCGTGTGGGTGGTCAATCATATACCACACAAGGCGGAGGAATGAAGA  
TTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCTCATCTCAGGGAAACGTT  
AGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACAGTTTGTACATCTTCAGGTGCTGG  
ATTTTTCTTACCACAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGC  
CACAGATCTGTTCTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGA  
TCCTTTTGAACATATCATACAGTTTGAGTCCCTGACCCAAGAACAGTTTAAATGGACCACTATGAGCCCACTTA  
CATAAAGAAAAAGGAGTGTACCCATGTTCTCATCCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATC  
GTGGCCTTCACATGTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTG  
TCTAAACAAGTCTCTTTAGATTTTGTAGTCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATCTTTTCATGGG  
TACCTTTGGAAGAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTTGGACAGCCATCAGATTGTCAGCC  
AAGAGCCTTTTATTTGAAAGCTCATTTCTTCCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGAC  
AGATTTTCAGGAAGAAAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACTACAGGACTCCAATTTTCAGTC  
TTATGACTTGGACACATAGACTGAATGAGACCAAGGAAAAAGCTTAACATACTACCTCAAGTGAACCTTTATTTA  
AAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAATGCTTTATTTATACAGAT  
GAACCAAAATTACAAAAAGTTATGAAAATTTTTTATACTGGGAATGATGCTCATATAAGAATACCTTTTAAACTA  
TTTTTTAACTTTGTTTTATGCAAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTT  
TTATAATGCCAGATTTCTTTTATGGAAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTT  
TTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAA

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## **FIGURE 102**

MVDVLLLFSLCLLFHISRFDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRNRI SAIPPKMFKL PQLOHLELNRNKIKNVDGLTFQGLGALKSLKM  
QRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE  
FCQKLSELDLTFNHL SRLDDSSFLGLSLNLT LHIGNNRVSYIADCAFRGLSSLKTLDLKNE  
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDSL DNAIMSLQGNAFSQ  
MKKLQQLHLNTSSLLCDCQLKWL PQWVAENNFSFVNASCAHPQLLKGRSIFAVSPDGFVCD  
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENY AHLRAQG  
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA  
MARLECAAVGHPAPQIAWQKDG GTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN  
SAGSISANATLTVLETPSFLRPLLDRTVT KGETAVLQCIAGGSPPKLNWTKDDSP LVVTER  
HFFAAGNQLLIIVDSDVSDAGKYTCEMSNTLGT ERGNVRLSVIPTPTCDSPQMTAPSLDDDG  
WATVG VVI IAVVCCVVGTS LVVWVVI IYHTRRRNEDCSITNTDET NLPADIPSYLSSQGT LAD  
RQDGYVSSSESGSHHQFVTSSGAGFFLPQH DSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP  
MYLKG NVYGS DPFETYHTGCSPDPRTV LMDHYEPSYIKKKECYPCSHPSEESCERSFSNISW  
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTL ENYRTPNFQS  
YDLDT

### **Signal sequence:**

amino acids 1-19

### **Transmembrane domain:**

amino acids 746-765

### **N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

### **Glycosaminoglycan attachment site.**

amino acids 826-830

### **Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

### **Tyrosine kinase phosphorylation site.**

amino acids 607-615

### **N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

[illegible]

GGGAGAGGAATTGACCATGTAAAAGGAGACCTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAAATG  
 AAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC  
 GAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA  
 TAAACCAGAGTTAGACCCGCGGGGTGGTGTGTTCTTGACATAAAATAAATAATCTTAAAGCAGCTGTTCCCTCC  
 CCACCCCAAAAAAAGGATGATTGGAATGAAGAACCGAGGATTCAAAAAGAAAAATGTTCATTTTCTC  
 TATAAGGAGAAAGTGAACCAAGGAGATATTTTTGGAAATGAAAAGTTTGGGGCTTTTTAGTAAAGTAAAGAACT  
 GTTGTGGTGGTGTTTTTCTTTCTTTTGAATTTCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAAGAAA  
 TTTTCAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA  
 TTTGTGCCTATGTTGACTAAATTTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTTTTTTTAAAT  
 TTTTATTCTTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCCTTAACCACCTGGATTTCATCTGGATGTTGCT  
 GTGATCAGTCTGAATAACAATCTGTTGAAATTCAGAGGACCAACACAGATCAAAATGATGAATGTTGAACAGAT  
 GACCTTACATCCACAGCAGATAATGATAGGCTCTAGGTTTTAACAGGGCCCTATTGACCCCTGCTTTGTGGTGTCT  
 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA  
 CCAGTTTCAGCAAGGTGATTTGTGTTTCGGA AAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCT  
 GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTTGGAATCTCT  
 ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTTGGGGCTTTTCAATGGTCTGGCGAACCTCAACACTCGGA  
 ACTCTTTGACAATCGCTTATCTACCATCCCCAATGGAGCTTTTGTATACTTGTCTAAACTGAAGGAGCTCTGGTT  
 GCGAAACAACCCCATGAAAGCATCCCTTCTTATGCTTTTAACGAAATTCCTTCTTTGCGCCGACTAGACTTAGG  
 GGAATTGAAAAGACTTTTCATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGC  
 CATGTGCAACCTTTCGGGAAATCCCTAACCTCACACCGCTCATAAACCTAGATGAGCTGGATCTTTCTGGGAATCA  
 TTTATCTGCCATCAGGCCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAACTGTGGATGATACAGTCCCAGAT  
 TCAAGTGATTGAACGGAATGCCCTTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACAATAATCTAAC  
 ATTAAGTGCCTCATGACCTCTTCACTCCCTTGCATCATCTAGAGCGGATACATTTACATCAACAACCTTTGGAACGT  
 TAACCTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCCGGTG  
 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTTCATGCTATGCTCCGGT  
 GATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAAGCTGAAATGTGCGGGCTCCACATC  
 CCTGACATCTGTATCTTGGATTCTCCAAATGGAACAGTTCATGACACATGGGGCGTACAAAGTCCGGATAGCTGTG  
 GCTCAGTGATGGTACGTTTAAATTTCAAAATGTAACCTGTGCAAGATACAGGCATGTACACATGATGTTGGTGAGTAA  
 TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCCTTTCTCTTACTTTTC  
 AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGTCCCACCTCC  
 AGTGGTGCAGCTGGGAGACCACCAATGTGACCACCTCTCTCACACCACAGAGCAAGGTGCAGACAGAGAAAACCTT  
 CACCATCCCAGTGACTGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT  
 TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTTCTACAAGATGAGGAAGCAGCACCA  
 TCGGCAAAACCATCACGCCCAACAAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC  
 CATGGAAGGCCACCTGCCCATGCCGTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT  
 CAACCACACAACAACAGTTAAACACAATAAATTCATACACAGTTTCAAGTGCATGAACCGTTATTTGATCCGAATGAA  
 CTCTAAAGACAATGTACAGAGACTCAAATCTAAACACATTTACAGAGTTTACAAAAACAACCAATCAAAAAAAA  
 GACAGTTTTATTAATAATGACACAATAATGACTGGGCTAAATCTACTGTTTCAAAAAGTGTCTTTACAAAAAACAA  
 AAAAGTAAAGAAATTTATTTTATTAATAAATTCATTGTGATCTAAAGCAGACAAAA

## **FIGURE 104**

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGI STNTRLLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNRLRYNLAMCNLREIPNLTPLIKLELDL SGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE  
LKCRASSTLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGN  
TTASATLNVTAATTTTFFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNTTSLTPQ  
STRSTEKTFTIPVTDINS GIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN  
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS  
VHEPLLIRMNSKDNVQETQI

### **Signal sequence:**

amino acids 1-44

### **Transmembrane domain:**

amino acids 523-543

### **N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

### **Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

### **N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537



## FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCA  
TGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGCAGCGCGAGGGAGGAGCGCGCACGCGACCGC  
GAGGGCGGGCGTGACCCCTCGGCTGGAAGTTTGTGCCGGGCCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGA  
GACCTAGGCCGCTGGACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTGGGGGCTGCTGCTGTGC  
GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGCGGTGCGGGGAACTCGGGCAGCCCTCTGGGGTAGCCGCC  
GAGCGCCATGCCCCACTACCTGCCGTGCCCTCGGGGACCTGCTGGACTGCAGTCGTAAGCGGCTAGCGCGTCTT  
CCCCGAGCCACTCCCGTCTGGGTGCTCGGCTGGACTTAAGTCACAACAGATTATCTTTTCATCAAGGCAAGTTCC  
ATGAGCCACCTTCAAAGCCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA  
GTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG  
TTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTAGAGCTCCAAACTGCATTTCCAGCCCTACAG  
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAAATTTGGCCAACACA  
CTCCTTGTTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAGATGTTTAAACTGCCCAACTGCAA  
CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGGTGCCTGAAAGTCT  
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGGCTGAGCAACATGGAAATTTTG  
CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCAT  
CTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA  
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATACACTGCACATTGGG  
AACACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAAC  
AATGAAATTTCTGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAAACTGAGGCGACTGATACCTC  
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCCTGAGT  
GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCAAAATGAAGAACTGCAACAATTCGATTTAAATACA  
TCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGTGGCGGAAAACAACTTTAGAGCTTTGTGTA  
AATGCCAGTTGTGCCCATCCTCAGCTGCTAAAAGGAAGAAGCATTTTGTGCTGTAGCCCAGATGGCTTTGTGTGT  
GATGATTTTCCCAAACCCAGATCACGGTTGAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC  
ATCTGCTCAGTGCCAGCAGCAGTGATTCCCAATGACTTTTGGCTTGAAAAAAGACAATGAACCTATGTCATGAT  
GCTGAAATGGAATTTATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACCACCATCCTTCGGCTG  
CGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCATCTCCAATCACTTTGGTTTCATCCTACTCTGTC  
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC  
ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGGCACAGAC  
TTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGACGTGTTCTTTATCGTGGATGTGAAGATA  
GAGGACATTTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTAGCAAAATGCAACTCTGACTGTC  
CTAGAAAACACCATCATTTTTCGGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGCTCTACAGTGC  
ATTGCTGGAGGAAGCCCTCCCCCTAACTGAACTGGACCAAAGATGATAGCCCATTTGGTGGTAACCGAGAGGCAC  
TTTTTTGAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTGATGCTGGGAAATACACATGTGAG  
ATGTCTAACACCCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCCT  
CAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCTGATCATAGCCGTGGTTTGTCTGT  
GTGGTGGGCACGTCACTCGTGTGGGTGGTTCATATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTACC  
AACACAGATGAGACCAACTTGCCAGCAGATATTCTAGTTATTTGTCTCATCTCAGGGAACGTTAGCTGACAGGCAG  
GATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACAGTTTGTACATCTTCAGGTGCTGGATTTTCTTACCA  
CAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTT  
CTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGATCCTTTTGAAACA  
TATCATAAGGTTGAGTCCCTGACCCAAGAAGCAGTTTTAATGGACCCTATGAGCCAGTTACATAAAGAAAAAG  
GAGTGCTACCCATGTTTCTCATCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCCTTCACAT  
GTGAGGAAGCTACTTAACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC  
TCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTTCATGGGTACCTTTGGAAAA  
GCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTTGGACAGCCATCAGATTGTCAGCCAAGAGCCCTTTTAT  
TTGAAAGCTCATTCTTCCCCAGACTTGGACTCTGGGTGAGGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAA  
GAAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC  
ACATAGACTGAATGAGACCAAGGAAAAGCTTAACATACTACCTCAAGTGAACTTTTATTTAAAAAGAGAGAGAAT  
CTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGCTTTATTTATACAGATGAACCAAAATTTAC  
AAAAAGTTATGAAAATTTTTTATACTGGGAATGATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTG  
TTTTATGCAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTTTATAATGCCAGA  
TTTCTTTTTATGGAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTTTTAAATAGAAGTT  
ACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAAERPCPTTCRCLGDLLDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT  
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFFPALQLKYLYLNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNRI SAIPPKMFKL PQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR  
NGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC  
QKLSELDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNEIS  
WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK  
KLQQLHLNTSSLLCDCQLKWL PQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDF  
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAHLRAQGGE  
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMPLPSFTKTPMDLTIRAGAMA  
RLECAAVGHAPQIAWQKDG GTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN SA  
GSISANATLTVLETSPFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTERHF  
FAAGNQLLIIVDSDVSDAGKYTCEMSNTLGTGRGNVRLSVIPTPTCDS PQMTAPSLDDDGWA  
TVGVVIIAVVCCVVGTSVLVWVVI IYHTRRRNEDCSITNTDETNPADIPSYLSSQGT LADRQ  
DGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY  
LKG NVYGS DPFETYHTGCSPDPRTV LMDHYEPSYIKKKECYPCSHPSEESCERSFSNISWPS  
HVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQ EENHICTFKQTL ENYRTPNFQSYDLDT

### **Signal sequence:**

amino acids 1-27

### **Transmembrane domain:**

amino acids 808-828

### **N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

### **Glycosaminoglycan attachment site.**

amino acids 886-890

### **Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085

### **Tyrosine kinase phosphorylation site.**

amino acids 667-675

### **N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

### **Leucine zipper pattern.**

amino acids 58-80, 65-87

## FIGURE 107

CAAAACCTTGCGTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCAGCTGAGAC  
TGGGGGAGCGCGTTTCGGCCTGTGGGGCGCCGCTCGGCGCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC  
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCTGGGTGGTCCCCTATCCCTCCTTTATATA  
GAAACCTTCCACACTGGGAAGGCAGCGGCGAGGCAGGAGGGCTCATGGTGAGCAAGGAGGCCGGCTGATCTGCAG  
GCGCACAGCATTCAGAGTTTACAGATTTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACAGCCTGCCTGGT  
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGCCGGGTGCTGC  
TGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGCCGTGAGGGCCCCAGGATTTGGCCGAA  
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTTGCGGAGGAGGAGCCGGTGCTGGTACTGAGCCCTGAGG  
AGCCCCGGCCTGGCCAGCCCGGTGAGCTGCCCCGAGACTGTGCTGTTCCAGGAGGGCGTCTGGACTGTG  
GCGGTATTGACCTGCGTGAGTTCCCGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGCAGAACAACCAGC  
TGGAAAAGATCTACCTTGAGGAGCTCTCCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAAACAACCGCCTGA  
CTTCCCGAGGGCTCCAGAGAAGGCGTTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC  
TGACCTTGGCACCCCGCTTCTGCCAAACGCCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAAGATCT  
ATGGGCTCACCTTTGGCCAGAAGCCAAACTTGAGGTCTGTGTACCTGCACAACAACAAGCTGGCAGACGCCGGGC  
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTGAGGTCTCATCTGTCCAGCAACTTCTGCGCCACGTGC  
CCAAGCACCTGCCGCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTGGAGAAGATCCCCCGGGGGCCT  
TCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAACAACCTACCTGACTGACGAGGGCCTGGACAACGAGA  
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCCAGCTGGGCTGC  
CGCGCAGCCTGGTGCTGCTGCACTTGAGAAGAACGCCATCCGGAGCGTGACCGGAATGTGCTGACCCCCATCC  
GCAGCCTGGAGTACCTGCTGTGTGCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCCACTGGCCTTCCAGGGCC  
TCAAGCGGTTGCACACGGTGACCTGTACAACAACCGCGCTGGAGCGCGTGCCAGTGGCCTGCCTCGCCGCGTGC  
GCACCCCTCATGATCCTGCACAACCAGATCACAGGCATTGGCCGGAAGACTTTGCCACCACCTACTTCTGGAGG  
AGCTCAACCTCAGCTACAACCGCATCACAGCCACAGGTGCACCGCGACGCCTTCCGCAAGCTGCGCCTGCTGC  
GCTCGCTGGACCTGTGCGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCTCGAAATGTCCATGTGCTGAAGG  
TCAAGCGCAATGAGCTGGCTGCCTTGGCAGGAGGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA  
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCCGTGCTGGGTGGACCTCGCCCATCTGCAGCTGCTGGACA  
TCGCGGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGAGTACCTGTACCTGCAGAACAACA  
AGATTAGTGCGGTGCCCGCCAATGCCCTTCGACTCCACGCCCAACCTCAAGGGGATCTTTCTCAGGTTTAAACAAGC  
TGGCTGTGGGCTCCGTTGGTGGACAGTGCCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGGACATTGAAGGCAACT  
TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGGAGG  
AGGAAGAGGAAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGGAATCTTTTCTGC  
AGCACACGCCTGTGTGCTGTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA  
TCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCACCGGCGTGTCCACGGCCAGACACATGC  
ACACACATCACACCTCAAACACCCAGCTCAGCCACACACAACCTACCTCAAACCACACAGTCTCTGTACAC  
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGGAAGGGTCTGCCCCCTGCCCTGGCACACACAGGCACCCA  
TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACCACACACACACATGCACAAGTCATGTGCGAA  
CAGCCCTCAAAGCCTATGCCACAGACAGCTCTTGCCCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCT  
GTCCATCTGTCCGTCCGTTCCCTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCCCTCT  
GGAACCTCACAAAAGCTGGCTTTTATTTCTTTCCCATCCTATGGGGACAGGAGCCTTCAGGACTGCTGGCCTGGCC  
TGGCCACCCCTGCTCCTCCAGGTGCTGGGCGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
CAGGCACCTTTTCCAATGGGCAAGCCAGTGGAGGCAGGATGGGAGAGCCCCCTGGGTGCTGCTGGGGCCTTGGGG  
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTTT  
GTTCTTCAGGCCTGTGGGGGAAGTCCGGGTGCCTTTATTTTATTCTTTCTAAGGAAAAAATGATAAAAAAT  
CTCAAAGCTGATTTTCTTGTATAGAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAA

## **FIGURE 108**

MEGEEAEQPAWFHQPWPRGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPREENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDCGGIDLREFFPGDLP  
EHTNHLSLQNNQLEKIYPEELSRLHRLETLNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK  
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV  
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN  
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMLHNQITGIGREDFATTYF  
LEELNLSYNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEEEEETR

### **Signal sequence:**

amino acids 1-48

### **N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

### **N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

### **Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

## FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTCTCCGGGAGCGGCAG  
CAGTAGCCCCGGGCGGCGAGGGCTGGGGGTTCTCGAGACTCTCAGAGGGGCGCCTCCCATCGGCGCCACCACCC  
CAACCTGTTCTCGCGCGCCACTGCGCTGCGCCCCAGGACCCGCTGCCAACATGGATTCTCTCTGGCGCTGGT  
GCTGGTATCCTCGCTCTACCTGCAGGCGGCGCCGAGTTTCGACGGGAGGTGGCCAGGCAAATAGTGTATCGAT  
TGGCCTATGTGCTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTTGGGACAGTGTGAGCC  
TGTGTGCCAACACGATGCAACATGGTGAATGTATCGGGCCAAACAAGTGCAAGTGTATCTCTGGTTATGCTGG  
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAACACAGGTGCATGAACACTTA  
CGGCAGCTACAAGTGTACTGTCTCAACGGATATATGCTCATGCCGGATGGTTCTCTGCTCAAGTGCCTTGACCTG  
CTCCATGGCAAACCTGTGAGTATGGCTGTGATGTTGTTAAAGGACAAATACGGTGGCAGTGCCCATCCCCCTGGCCT  
GCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCCTGCCCTAGATT  
TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTATATAAGGCTTCGATCTCATGTATATTGGAGG  
CAAATATCAATGTATGACATAGACGAATGCTCACTTGGTCAAGTGTATGAGTGCAGCAGCTTTGCTCGATGTTATAA  
CGTACGTGGGTCTTACAAGTGCAAATGTAAAGAAGGATACAGGGTGATGGACTGACTTGTGTGTATATCCAAA  
AGTTATGATTGAACCTTCAGGTCCAATTTCATGTACCAAAGGGAAATGGTACCATTTTAAAGGGTGACACAGGAAA  
TAATAATTGGATTCTGATGTTGGAAGTACTTGGTGGCCTCCGAAGACACCATATATTCCTCCTATCATTACCAA  
CAGGCCTACTTCTAAGCCAACAACAAGACCTACACCAAAGCCAACCAATTCTACTCCACCACCACCACCACC  
CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAGGCCAACCACCGGACTGACAACCTATAGC  
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACCCCTCAGAAAACCCAGAGG  
AGATGTGTTTCAAGTGTCTGGTACACAGTTGTAATTTTGACCATGGACTTTGTGGATGGATCAGGGAGAAAGACAA  
TGACTTGCACCTGGGAACCAATCAGGGACCCAGCGAGTGACAAATATCTGACAGTGTCCGCAGCCAAAGCCCCAGG  
GGGAAAAGCTGCACGCTTGGTGCTACCTCTCGGCCGCTCATGCATTTCAGGGGACCTGTGCTGTGCTTTCAGGCA  
CAAGGTGACGGGGCTGCACCTCTGGCACACTCCAGGTGTTTGTGAGAAAAACCGGTGCCCCAGGAGCAGCCCTGTG  
GGGAAGAAATGGTGGCCATGGCTGGAGGCAACACAGATCACCTTGCAGGGGCTGACATCAAGAGCGAATCACA  
AAGATGATTAAAGGGTTGGAAGAAAAAGATCTATGATGGAAAAATTAAGGAACTGGGATTATTGAGCCTGGAGAAG  
AGAAGACTGAGGGGCAAACCATTGATGGTTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCGACCAGCTG  
TTCTCCATATGCACTAAGAATAGAACAAGAGGAACTGGCTTAGACTAGAGTATAAGGGAGCATTTCTTGGCAGG  
GGCCATTGTTAGAATACTTCATAAAAAAGAGTGTGAAAAATCTCAGTATCTCTCTCTCTTTCTAAAAAATTAGA  
TAAAAATTTGTCTATTTAAGATGGTTAAAGATGTTCTTACCCAAGGAAAAAGTAACAAATTATAGAATTTCCAAA  
AGATGTTTTGATCCTACTAGTAGTATGCAGTGAAAACTTTAGAACTAAATAATTTGGACAAGGCTTAATTTAGG  
CATTTCCCTCTTGACCTCCTAATGGAGAGGGATTGAAAAGGGGAGAGCCCCACCAAATGCTGAGCTCACTGAAATA  
TCTCTCCCTTATGGCAATCCTAGCAGTATTAAGAAAAAGGAACTATTTATTTCAAATGAGAGTATGATGGAC  
AGATATTTTAGTATCTCAGTAATGTCTAGTGTGGCGGTGGTTTTCAATGTTTCTTCATGGTAAAGGTATAAGCC  
TTTCATTTGTTCAATGGATGATGTTTCAGATTTTTTTTTTTTTTAAGAGATCCTTCAAGGAACACAGTTTCAGAGAG  
ATTTTCATCGGGTGCAATCTCTCTGCTTCGTGTGTGACAAAGTTATCTTGGCTGCTGAGAAAGAGTGCCCTGCCCC  
ACACCGGCAGACCTTTCTCTCACCTCATCAGTATGATTGAGTTTCTCTTATCAATTGGACTCTCCAGGTTCCAC  
AGAACAGTAATATTTTTGAACAATAGGTACAATAGAAGGTCTTCTGTGATTTAACCTGGTAAAGGCAGGGCTGG  
AGGGGAAAAATAAATCATTAAGCCTTTGAGTAACGGCAGAATATATGGCTGTAGATCCATTTTAAATGGTTTATT  
TCCTTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGGAAAAATAAATGAAAAATTTTACTTTTCGATGCCAA  
TGATACATTGCACATAAAGTATGGAAGAGTTATCCAAAGTACTGTATAACATCTTGTATTATTATTTAATGTTTT  
CTAAAAATAAAAAATGTTAGTGGTTTTTCCAATGGCCTAATAAAAACAATTATTTGTAAATAAAAAACTGTAGTAAT

## **FIGURE 110**

MDFLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP  
RCKHGEICIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPLHLAPDGRTCVDVDECATGRASCPRFRQC  
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHVPKGNLTILKGD TGNNNWIPDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPLPTLRTPLPPTTPERPTTGLTTIAPAASPPGGITVDN  
RVQTDPOKPRGDVFSVLVHSCNFDHGLCGWIREKDNLDLHWEPIRDPAGGQYLTVSAAKAPGG  
KAARLVLPGLRLMHSGDLCLSFHVKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI  
TLRGADIKSESQR

### **Signal sequence:**

amino acids 1-17

### **N-glycosylation site.**

amino acids 273-277

### **Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

### **Tyrosine kinase phosphorylation site.**

amino acids 199-206

### **N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

### **Cell attachment sequence.**

amino acids 382-385

### **EGF-like domain cysteine pattern signature.**

amino acids 75-87

## FIGURE 111

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCTTTAGATTGTGA  
AATGTGGCTCAAGGTCTTCACAACCTTTCTTTCTTTGCAACAGGTGCTTGCTCGGGGCTGA  
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA  
CACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCTGACTTGGAATACC  
AACACAAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTT  
GATGAAGGCAATTACATCGTGAAGGTCAACATTTCAGGGAAATGGAATCTATCTGCCAGTCA  
GAAGATACAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTATCCTCCCT  
CTGGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGG  
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC  
TCCCCAAAACAATACCTTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT  
GCCTGGTGAGGAACCTGTGAGTGAATGGAAGTGATATCATTATGCCCATCATATATTAT  
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT  
TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAGCATGGGCCTCGCTTAGAAGTT  
GCATCTGAGAAAGTAGCCAGAACACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC  
CGGCAGGCAAGATGAAACTCATTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG  
CACAGAAAGGAAAATCATTTGTACCTTTAGCAAGTATAACTGGAATATCACTATTTTTTGATT  
ATATCCATGTGTCTTCTCTTCTATGGAAAAATATCAACCCTACAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGCCAGAAACAGAAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATG  
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT  
GTATGAAGTTATTCAGCACATCCCTGCCAGCAGCAAGACCATCCAGAGTGAACCTTTTCATGG  
GCTAAACAGTACATTCGAGTGAATTTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAAAGT  
ATATTAATCTGGAATCAGTGAAGAAACAGGACCAACACCTCTTACTCATTATTCCTTTACA  
TGCAGAATAGAGGCATTTATGCAAATTGAACTGCAGGTTTTTTCAGCATATACACAATGTCTT  
GTGCAACAGAAAAACATGTTGGGGAAATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGG  
GGAGAACGAAAGTGACAGGGGTTTCTCATAAGTTTGTATGAAATATCTCTACAAACCTCA  
ATTAGTTCTACTCTACACTTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA  
TGTGGAACTTTACATTGTTTCGATTTTTCAGCAGACTTTGTTTTATTAAATTTTTTATTAGTG  
TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTTATTTGTACAA  
CAAAGTAATAAGGATGGTTGTCAAAAAACAAACTATGCCTTCTCTTTTTTTTCAATCACC  
AGTAGTATTTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTAA  
TTTTTTTCAAGGAAAGATGGATTCAAATAAATATTCTGTTTTTGCTTTTAAAAA

## **FIGURE 112**

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTLSASQ  
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPPIIYYGPYGLQVNSDKGLKVGEVFTV  
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTV  
YEVIQHIPAQQQDHPE

### **Signal sequence:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 341-359

### **N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

### **Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

### **Tyrosine kinase phosphorylation site.**

amino acids 272-280

### **N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

FIGURE 112



## FIGURE 113

GCAAGCGGCGAAATGCGGCCCTCCGGGAGTCTTGCAGTTCCCCTGGCAGTCCTGGTGCTGTT  
GCTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTGCGGTCATCACGGACGAGA  
ACTGGAGAGAAGTCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCT  
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTTGCTGAATGGGGAGAAGATCTTGAGGTTAA  
TATTGCGAAAGTAGATGTACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC  
TTCCTACTATTTATCATTTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG  
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGAAGAGTATTGAGCCCGTTTCATCATG  
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT  
GTTTTTGCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC  
AGATTGCCTTTGTCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTTCAAAAAAAT  
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA  
GATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTTCCACAGAATGC  
CATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAATCCTAGTTAAATTTTATAG  
TTATCTTAATATTATGATTTTGATAAAAACAGAAGATTGATCATTTTGTTTGTTTGAAGTG  
AACTGTGACTTTTTTTGAATATTGCAGGGTTTCTAGTCTAGATTGTCATTAAATTGAAGAGTCTA  
CATTTCAGAACATAAAGCACTAGGTATACAAGTTTGAAATATGATTTAAGCACAGTATGATG  
GTTTAAATAGTTCTCTAATTTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTTGT  
TTAATAATAACCTATTTCAAGTCTGAGTTTTGAAAAATTTACATTTCCCAAGTATTGCATTAT  
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTTCTCTG  
TTTCACTGTGTGAAAAAAGAAGATATTTCCCATAAATGGGAAGTTTGCCCATTTGTCTCAAG  
AAATGTGTATTTTCAGTGACAATTTCTGTGGTCTTTTTTAGAGGTATATTCCAAATTTCTTGT  
ATTTTTAGGTTATGCAACTAATAAAAACTACCTTACATTAATTAATTACAGTTTTCTACACA  
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATTC  
CAACAAAGTTTGATTTTCTCTTGATTTTTCTTACTTACTATGGGTACATTTTTTTATTTTT  
CAAATTGGATGATAATTTCTTGAAACATTTTTTATGTTTTAGTAAACAGTATTTTTTTGTT  
GTTTCAAAGTGAAGTTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTTAAATTT  
TTGGCCACTTTTTTCAGATTTTACATCATTTCTTGCTGAACCTTCAACTTGAAATGTTTTTTTT  
TTTCTTTTTTGGATGTGAAGGTGAACATTCCTGATTTTTGTCTGATGTGAAAAAGCCTTGGTA  
TTTTACATTTTGAAAATTCAAAGAAGCTTAATATAAAAAGTTTGCAATTCTACTCAGGAAAAAG  
CATCTTCTTGATATATGTCTTAAATGTATTTTTGTCTCATATACAGAAAGTTCTTAATTGAT  
TTTACAGTCTGTAATGCTTGATGTTTTAAAATAATAACATTTTTTATATTTTTTAAAAGACAA  
ACTTCATATTATCCTGTGTTCTTTCCTGACTGGTAATATTGTGTGGGATTTTACAGGTAAAA  
GTCAGTAGGATGGAACATTTTAGTGATTTTTTACTCCTTAAAGAGCTAGAATACATAGTTTT  
CACCTTAAAGAAGGGGGGAAAATCATAAATACAATGAATCAACTGACCATTACGTAGTAGAC  
AATTTCTGTAATGTCCCCTTCTTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTTACAG  
TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAATATTGTACCATT  
AAAGAGTTTGGATGTGTAACCTGTGATGCCTTAGAAAAATATCCTAAGCACAAAATAAACCT  
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAAAAAAAA

CCCTGCTGTT

## **FIGURE 114**

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFISDKEWKSIIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEQEAEDEEDVSE  
EEAESKEGTNKDFPQNAIRQPSLGPSLATDKS

### **Signal sequence:**

amino acids 1-26

### **Transmembrane domain:**

amino acids 182-201

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

### **Tyrosine kinase phosphorylation site.**

amino acids 107-115

### **N-myristoylation site.**

amino acids 20-26, 192-198

### **Amidation site.**

amino acids 25-29

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
Male	55.2 (10.5)
Female	58.5 (11.2)
Marital status	
Married	78.5%
Single	21.5%
Education level	
High school or less	65.2%
College or more	34.8%
Occupation	
Professional	45.5%
Managerial	25.5%
Technical	15.5%
Service	13.5%
Unemployed	9.5%
Income (USD/month)	
< 1000	15.5%
1000-2000	35.5%
2000-3000	25.5%
> 3000	23.5%
Health insurance	
Yes	85.5%
No	14.5%
Smoking status	
Smoker	35.5%
Non-smoker	64.5%
Alcohol consumption	
Yes	15.5%
No	84.5%
Family size	
1-2	45.5%
3-4	35.5%
5 or more	19.0%

CGCAGTGTGTCAGAGTGC GGAGACCCGTGATAATT CGTTAACTAATTCAACAAACGGGACCCCTT  
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG  
AAGGTCCTGGCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC  
ATTGCTGATGGCCTGGTTTGGTGTCTTGAGCTGTGTGCAGGCCGAATTCTTCACCTCTATTG  
GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC  
CTTGTGGAGGAAGCCAAGCTTTC AAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC  
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCCCTGTGAATGCCTACAAACTGG  
TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTCTGCAGGACTCAGCTGCA  
GGTTTTATCGCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGG  
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA  
GAGGGGAACCTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG  
GGCCGCTCGCGCTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT  
AAAGCAGCTTGATGCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA  
GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCTTGCTC  
TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA  
GGAAGAGAGAGAAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAGGCA  
TCTATGAGAGGCCTGTGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGTGGG  
GAGGGTGTCAAAC TGACACCCCGTAGACAGAGAGGCTTTTCTGTAGGTACCACCATGGCAA  
CAGGGCCCCACAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCCGCACA  
TCGT CAGGTACTACGATGT CATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA  
CCTAAACTTGACAGAGCCACCGTTCTGTGATCCCAAGACAGGAGTCCCTCACTGT CGCCAGCTA  
CCGGGTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCTGTTGTGGCCCCGAGTAAATC  
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTGTTACAGGTTGCAAAT  
TATGGAGTGGGAGGACAGTATGAACCGCACCTTCGACTTCTCTAGCGGACCTTTTGACAGCGG  
CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGATGTAGAAGCTG  
GTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG  
TTCTGGTACAACCTCTTGCGGAGCGGGGAAGGTGACTACCGAACAAGACATGCTGCCTGCC  
TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTTGTGGATCAACAGAAGTTGACTGA CATCCTTTTCTGTCTCTCCCCCTTCCCTGGTC  
CTTCAGCCCATGTCAACGTGACAGACACCTTTGTATGTTCCCTTTGTATGTTCCCTATCAGGCT  
GATTTTTTGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT  
GTGACTGAAGTCCAGCCCTTCCATT CAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA  
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTT CAGTGAACCAAAGTTCTGATACCTTGTTTACATGTTTGT TTTTAT  
GGCATTTCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAGAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQRQFFP  
TDEDEIGAALKMRLQDTYRLDPGTISRGLPGTKYQAMLSVDDCFGMGRSAYNEGDIYHTV  
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR  
YFEQLLEEEREKTLTNQTEAELATPEGIYERPVLYLPERDVYESLCRGEVGLTPRRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPIVRYDVMSDEEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDPS  
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGECDYR  
TRHAACPVLVGCKWVSNKWFHERGQEFLLRPGSTEVD

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

## FIGURE 117

GCAGTATTGAGTTTTACTTCCTCCTCTTTTTAGTGGAAGACAGACCATAATCCCAGTGTGAGTGAAATTGATTGT  
TTCATTTATTACCGTTTTGGCTGGGGGTAGTTCCGACACCTTTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA  
AGACAGGACAATCTTCTGGGGATGCTGGTCTGGAAGCCAGCGGGCCTTGCTCTGTCTTTGGCCTCATTGACCC  
CAGGTTCTCTGGTTAAAACTGAAAGCCTACTACTGGCCTGGTGCCCATCAATCCATTGATCCTTGAGGCTGTGCC  
CCTGGGGCACCCACCTGGCAGGGCCTACCACCATGCGACTGAGCTCCCTGTTGGCTCTGCTGCGGCCAGCGCTTC  
CCCTCATCTTAGGGCTGTCTCTGGGGTGACGCTGAGCCTCCTGCGGGTTTTCTGGATCCAGGGGGAGGGAGAAG  
ATCCCTGTGTGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG  
ATGAAGACTTCAAACCCCGGATTGTCCCCTACTACAGGGACCCCAACAAGCCCTACAAGAAGGTGCTCAGGACTC  
GGTACATCCAGACAGAGCTGGGCTCCCGTGAGCGGTTGTGGTGGCTGTCTGACCTCCCGAGCTACACTGTCCA  
CTTTGGCCGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCCTCGGTTACTCTACTTCACTGGGCAGCGGGGG  
CCCCGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGGATGAGCGGCCCGCCTGGCTCATGTGAGAGACCCCTGC  
GCCACCTTCACACACACTTTGGGGCCGACTACGACTGGTTCTTCATCATGCAGGATGACACATATGTGCAGGCCC  
CCCGCCTGGCAGCCCTTGCTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGGCAGAGGAGTTTATTG  
GCGCAGGCGAGCAGGCCCGGTACTGTCTATGGGGCTTTGGCTACCTGTTGTACGGAGTCTCCTGCTTCGTCTGC  
GGCCACATCTGGATGGCTGCCGAGGAGACATTCTCAGTGCCCGTCCCTGACGAGTGGCTTGGACGCTGCCCTCATTG  
ACTCTCTGGGCGTCGGCTGTGTCTCACAGCACCAGGGGCAGCAGTATCGCTCATTTGAACTGGCCAAAAATAGGG  
ACCCTGAGAAGGAAGGGAGCTCGGCTTTCTGAGTGCCTTCGCCGTGCACCCTGTCTCCGAAGGTACCCCTCATGT  
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAATAGAACAACTGCAGGCTCAGA  
TCCGGAACCTGACCGTGCTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCCGTGGGGTCCCTGCTCCTTTCA  
CACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGCACACCTTCTCCTGTGCAGATGGGG  
CTCCCAAGTGCCCACTACAGGGGGCTAGCAGGGCGGACGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA  
ATCGGCGCTATCAGCCCCGCTGCGCTTCAGAAGCAGCGACTGCTCAACGGCTATCGGCGCTTCGACCCAGCAC  
GGGGCATGGAGTACACCTGGACCTGCTGTTGGAATGTGTGACACAGCGTGGGCACCGGCGGGCCCTGGCTCGCA  
GGGTGAGCCTGCTGCGGCCACTGAGCCGGGTGGAATCCTACCTATGCCCTATGTCACTGAGGCCACCCGAGTGC  
AGCTGGTGCTGCCACTCCTGGTGGCTGAAGCTGCTGCAGCCCCGGCTTTCTCGAGGCGTTTGCAGCCAAATGTCC  
TGGAGCCACGAGAACATGCATTGCTCACCTGTTGCTGGTCTACGGGCCACGAGAAGGTGGCCGTGGAGCTCCAG  
ACCCATTTCTTGGGGTGAAGGCTGCAGCAGCGGAGTTAGAGCGACGCTACCTGGGACGAGGCTGGCCTGGCTCG  
CTGTGCGAGCAGAGGCCCCCTTCCAGGTGCGACTCATGGACGTGGTCTCGAAGAAGCACCCCTGTGGACACTCTCT  
TCTTCCTTACCACCGTGTGGACAAGGCCTGGGCCCGAAGTCCCTCAACCGCTGTGCGATGAATGCCATCTCTGGCT  
GGCAGGCCTTCTTTCCAGTCCATTTCCAGGAGTTCAATCCTGCCCTGTCAACACAGAGATCACCCCCAGGGCCCC  
CGGGGGCTGGCCCTGACCCCCCTCCCTCCTGGTGCTGACCCCTCCCGGGGGCTCCTATAGGGGGGAGATTTG  
ACCGGCAGGCTTCTGCGGAGGGCTGCTTCTACAACGCTGACTACCTGGCGGCCCGAGCCCGGCTGGCAGGTGAAC  
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGGGCTGGAGGTGATGGATGTTTCTCCTCCGGTTCTCAGGGCTCC  
ACCTCTTTTGGGGCCGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAGCCCACGGCTCAGTGAAG  
AACTCTACCACCGCTGCCGCCCTCAGCAACCTGGAGGGGCTAGGGGGCCGTGCCAGCTGGCTATGGCTCTCTTG  
AGCAGGAGCAGGCCAATAGCACTTAGCCCCGCTGGGGGCCCTAACCTCATTACCTTTCTTTGTCTGCCTCAGCC  
CCAGGAAGGGCAAGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTTTAAATATGAAATGTTATTAA  
ACATGTCTTCTGCC

DETAILED

## **FIGURE 118**

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQEGEDPCVEAVGERGGPQNPD SRARLD  
QSDedFKPRIVPYRDPNKPYPKKVLRTRYIQTELGSRRERLLVAVLTSRATLSTLAVAVNRTV  
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG  
DILSARPDEWLGRCLIDSLGVGCVSQHQQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEV  
LGWDYFTEQHTFSCADGAPKCPLOGASRADVGDALETALEQLNRRYQPRLRFOKQRLNNGYR  
RFDPARGMEYTLDLLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLP  
VAEAAAAPAFLEAFAANVLEPREHALLTLLL VYGPREGGRGAPDPFLGVKAAAELERRYPG  
TRLAWLAVRAEAPSQVRLMDVVS KKHVPDTLFFLT TVWTRPGPEVLNRCRMNAISGWQAFFP  
VHFQEFNPALSPQRSPPGPPGAGPDPPSPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA  
RARLAGELAGQEEEEALEGLEVMDFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRAQLAMALFEQE QANST

### **Signal sequence:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 489-507

### **N-glycosylation site.**

amino acids 121-125, 342-346

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

### **Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

### **Tyrosine kinase phosphorylation site.**

amino acids 736-743

### **N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

### **Cell attachment sequence.**

amino acids 247-250

## FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCC  
GTTCTAGACGCGGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG  
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAAATTTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAAAACC  
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG  
AGTTCTTCAGTTCTGAAAATGTTAAAGTGTTTGAGTCAATTAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACCTG  
GTTCTTCCTTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTTGTTAA  
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT  
CAATATCCCAGAAAAGTGTCCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTTAATACCAAATCTGTTGGGCTTCTATTAAAGAGGCAATGACTTATCACCC  
CAACCAGGTAGTAGAAGGCTGTTGTTTCAAGATATGGCTGTTACTTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTTGGGCATATTTTCAAT  
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACTACATATCCAA  
TACAGCTGTATGTTTCTTTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTCTTTAAACACATGAACATTGTAAATG  
TGTTGGAAAGAAGTGTTTTAAGAATAATAATTTTGCAAATAAACTATTAATAAATATTATAT  
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTGTCTGATTGGTT  
AAAAAATTTTAACAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAAACCTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT  
AAGCCTCCCCAAGTTCCAATGGATTTGCCTTCTCAAATGTACAATAAGCAACTAAAGAAA  
ATTAAAGTGAAAGTTGAAAAAT

## **FIGURE 120**

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAI IENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG  
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

### **Signal sequence:**

amino acids 1-33

### **N-glycosylation site.**

amino acids 121-125, 342-346

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

### **Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

### **Tyrosine kinase phosphorylation site.**

amino acids 736-743

### **N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

### **Cell attachment sequence.**

amino acids 247-250

FIGURE 120



## FIGURE 121

CCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG  
AAAAAGAGAGAGAGAGAGAAACAAAAAACCAAAGAGAGAGAGAAAAAATGAATTCATCTAAATCAT  
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCCAAATGTTCTTATGGACTGTTGCT  
GGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTTCGCAT  
CTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTACAGAGCTCTCCTGCT  
ACAATTATGGATCAGGTTTCAGTCAAGAATTGTTGTCCATTGAACTGGGAATATTTTCAATCC  
AGCTGCTACTTCTTTTCTACTGACACCATTTCCTGGGCGTTAAGTTTAAAGAACTGCTCAGC  
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCCTACAAGA  
AACCTAAAATGAGAGAGTTTTTTTATTGGACTGTCAGACCAGGTTGTGCGAGGGTCAGTGGCAA  
TGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA  
CATAGCTACCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAATTTGGA  
ATGATGTAACCTGTTTCCTCAATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTG  
AACAAAGGAAAATCTCTTTAAAGAACAGAAGGCACAACCTCAAATGTGTAAAGAAGGAAGAGCA  
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTTGTGCGCTGAACTTCAAAGGACTTC  
ATAAGTATTTGTTACTCTGATACAAATAAAAATAAGTAGTTTAAATGTTAAAAAAAAAAAAA  
AA  
AAAAA

## **FIGURE 122**

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDCAATMRDSS  
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

### **Signal sequence:**

amino acids 1-42

### **N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

### **N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

090445 07130  
T00T20"294060

## FIGURE 123

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCCTGCTGCTGCTTTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAAGTGTCTTGATCATTTACGGATTTCGC  
AGACAAGTGACCCAGGATCGAGTGAAGAAAATTCAGATGAACAAACCATATGTGTTTTTTGACAAACAAA  
TTCAGGGAGACTTGGCGGGTCTGTCAGAAATCTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTTATCGCTGTGAGGTCTGTCGAAATGACCGCAAGGAAATTTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGTAGGGGCCACCCCGGCCCTCACTACAGCTGGTATCGCAATGATGTACCAGTGCACCGGATT  
CCAGAGCCAATCCAGATTTTCGCAATTTCTTTTCCACTTAAACTCTGAAACAGGCACTTTGGTGTTCAGTGTCTG  
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGCGGAAATTAATGGGGGGTTCGTGTTGTCTTGCTGTACTGGCCCTGA  
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTTCATCAACAATAAACAGGATGGAGAAAAGTTACAAGA  
ACCCAGGAAACAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG  
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA  
GGCAGCGAGAGCTGATGCACCTCGGACAGAGCTAGACACTCATTCAGAAGCTTTTCGTTTGGCCAAAGTTGACCA  
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCCTCAAGATGGACCCGGTAAATATAACACAA  
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCCTAATCTGTTTCTGGCCTGATTCCCGCATGAGTATTAGG  
GTGATCTTAAAGAGTTTGTCTACGTAAACGCCCGTGTGGGCCCTGTGAAGCCAGCATGTTTACCAGTGGTCTGT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGGCGGGAAACCA  
GAAAAGGCTTCTTACACAGCAGCCTTACTTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCAAGTGTCCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAGGAAG  
GTAAATTGGTTGCTGGAAGAGGGATCTTGCTGAGGAACCTGCTTGTCCAACAGGGGTGTGAGGATTTAAGGAAA  
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTATTATTTATAAAATTT  
TACATCTAAATTTTGTCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAAACTGTAAATATATTGT  
CATACAATGTTAAATAACCTATTTTTTTTAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTAAAT  
TGGAATAATCAATAATTAAGAGTATTTTACCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTTCTTTTCT  
CACACAAGTTTTTAGCCTTTTTTCAACAAGGGAACCTACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAAATCCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT  
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG  
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT  
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGCTTTCATCCAGCACAGC  
TCTCAGGTGGGCACTGCAGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTAAACAGACCTCT  
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTTAAAGTTTGTTTAATTATTGTT  
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT  
CCCAGTGTCTCTTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCAATTTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAAG  
TGAAACGCCCTGAATCAAAAGCAGTTTCTAATTTTGACTTTAAATTTTTTCATCCGCCGGAGACACTGCTCCCATT  
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCTGGA  
GAATGGCTCTCACTACTCACCTTGTCTTTTTCAGCTTCCAGTGTCTTGGGTTTTTTTATACTTTTGACAGCTTTTTTTT  
AATTGCATACATGAGACTGTGTTGACTTTTTTTTAGTTATGTGAAACACTTTGCCGCAGGCCGCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGTCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATTTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCTCAGCGTTGGGGATTACGCTCCAGCCTCCT  
TCTTGGTTGTATAGTGTATAGGGTAGCCTTATTGCCCTTCTTCTTATACCTTAAACCTTCTACACTAGTGCCA  
TGGAACAGGCTCTGAAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTTGGCATTGTGTTAAC  
CTCATTTATAAAAGCTTCAAAAAACCCA

## **FIGURE 124**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS  
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK  
EIDEIVIELTVQVKPVTVCVRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPTDSRA  
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDNLNIGGIIGG  
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-30

#### **Transmembrane domain:**

amino acids 243-263

#### **N-glycosylation sites.**

amino acids 104-107, 192-195

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

#### **Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

#### **Tyrosine kinase phosphorylation site.**

amino acids 69-77

#### **N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267